

SEQUENCE LISTING

<110> Kleanthous, Harold
Al-Garawi, Amal
Miller, Charles
Tomb, Jean Francois
Oomen, Raymond P.

<120> IDENTIFICATION OF POLYNUCLEOTIDES
ENCODING NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER
GENOME

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Glu	Asn	Trp 195	Asp	His	Leu	Lys	Phe 200	Pro	Arg	Ser	Val 205	Leu	Gly	Arg	Arg
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Ser	Tyr 290	Tyr	Ser	Ala 295	Thr	Val	Gly	Ser	Phe	Val 300	Gly	Ala	Asp	Phe	Asn
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Ala 465	Gly	Gly	Phe	Arg 470	Asn	Asp	Glu	Leu	Val	Leu 475	Val	Ser	Tyr	Glu	Asn
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Tyr Ile Thr Gln Gly Val Asp Ser Ser His Ile Val Asp Gly Lys Lys	
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Thr Glu Glu Ile Glu Lys Ile Ala Thr Lys Arg Ala Thr Ile Arg Val	
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Gln Pro Ile Tyr Asp Ser Leu Met Asn Val Asp Arg Leu Gly Ile Tyr	
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 Ser Glu Tyr Ile Thr Gln Gly Val Asp Ser Ser His Ile Val Asp Gly
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 Lys Lys Thr Glu Glu Ile Glu Lys Ile Ala Thr Lys Arg Ala Thr Ile
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 Ile Val Phe Phe Gly Thr Met Gly Phe Lys Lys Leu Ser Val Ala Leu
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 Phe Pro Lys Ile Asp Leu Pro Thr Val Val Val Thr Thr Thr Tyr Pro
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 Gly Ala Ser Ala Glu Ile Ile Glu Ser Lys Val Thr Asp Lys Ile Glu

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Ser	Lys	Asn	Val	Ser	Ile	Val	Val	Ile	Glu	Phe	Glu	Leu	Glu	Lys	Pro				
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Leu	Glu	Ser	Arg	Tyr	Thr	Lys	Leu	Leu	Gln	Trp	Val	Leu	Asn	His	Lys	
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2386

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Leu	Leu	Leu	Leu	Lys 1045	Gly	Pro	Pro	Lys	Ile 1050	Phe	Phe	Leu	Leu	Leu 1055	Gly	
Lys	Gly	Gly	Ile 1060	Glu	Lys	Lys	Phe	Trp 1065	Trp	Trp	Trp	Trp	Lys 1070	Arg	Phe	

Phe	Gly	Met	Met	Leu	Ser	Asn	Asn	His	Leu	Arg	Ala	Ala	Asn	Asp	Asn
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Glu	Ser	Ala	Ala	Ser	Ala	Phe	Phe	Lys	Arg	Arg	Arg	Arg	Arg	His	Gly
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Cys	Arg	Arg	Arg	Arg	Arg	Phe	His	Gln	Gln	Thr	Gly	Gly	Gly	Lys	Gln
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Gln	Leu	Glu	Phe	Phe	Leu	Pro	Pro	Asn	Phe	Val	Val	Val	Val	Val	Gly
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Gln	Asn	Ser	Ser	Ser	Trp	Leu	Leu	Ser	Ala	Gly	Gly	Ala	Ala	Leu	Val
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Tyr	Tyr	Gln	Gly	Gly	Arg	Leu	His	His	Cys	Leu	Asn	Asn	Leu	Gln	Gln
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Lys	Thr	Thr	Ile	Ile	Ile	Ile	Ile	Thr	Leu	Leu	Phe	Arg	Ala	Ala	Thr			
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Asn	Ala	Lys	Lys	His	Ala	Leu	Leu	Val	Met	Met	Asn	Gln	Ile	Ile	Ile			
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Trp	Phe	Lys	Asp	Asp	Ser	Gly	Ala	Ala	Trp	Cys	Cys	Ser	Ser	Ile	Ile			
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gct atg att	aat aga	gcg acc	tta cac	aat tat	tct gaa	att gaa	aaa									168
Met Ile Asn	Arg Ala	Thr Leu	His Asn	Tyr Ser	Glu Ile	Glu Lys										
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Lys Asn Ile	Met Leu	Ser Asp	Arg Val	Val Val	Ile Arg	Ser Gly	Asp									
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Val Ile Pro Lys Ile Ile Lys Pro Leu Glu Ser Tyr Arg Asp Gly Ser
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caa cat aaa att gaa cgc ccc aag gtt tgc cct ata tgt tcg cat gag      312
Gln His Lys Ile Glu Arg Pro Lys Val Cys Pro Ile Cys Ser His Glu
          50                55                60

ctt ttg tgc gaa gag att ttt act tat tgt caa aac ctt aat tgc ccg      360
Leu Leu Cys Glu Glu Ile Phe Thr Tyr Cys Gln Asn Leu Asn Cys Pro
          65                70                75

gca agg ttg aaa gaa agc ttg att cat ttc gct tct aaa gac gct tta      408
Ala Arg Leu Lys Glu Ser Leu Ile His Phe Ala Ser Lys Asp Ala Leu
          80                85                90                95

aac att caa ggc ttg ggc gat aaa gtc ata gag caa ctt ttt gaa gaa      456
Asn Ile Gln Gly Leu Gly Asp Lys Val Ile Glu Gln Leu Phe Glu Glu
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aag ctc att ttt aac gct ctg gat ttg tat gct tta aaa tta gaa gat      504
Lys Leu Ile Phe Asn Ala Leu Asp Leu Tyr Ala Leu Lys Leu Glu Asp
          115               120               125

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Leu Met Arg Leu Asp Lys Phe Lys Ile Lys Lys Ala Gln Asn Leu Leu
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gac gct att tta aaa agc aaa aac cct ccc tta tgg cgt ttg att aac      600
Asp Ala Ile Leu Lys Ser Lys Asn Pro Pro Leu Trp Arg Leu Ile Asn
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Ala Leu Gly Ile Glu His Ile Gly Lys Gly Ala Ser Lys Thr Leu Ala
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Lys Tyr Gly Leu Asn Val Leu Glu Lys Ser Glu Xaa Ser Phe
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His Lys Ile Glu Arg Pro Lys Val Cys Pro Ile Cys Ser His Glu Leu
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Leu Cys Glu Glu Ile Phe Thr Tyr Cys Gln Asn Leu Asn Cys Pro Ala

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Overall Sample		Non-Indigenous		Indigenous		
Variable	Mean	SD	Mean	SD	Mean	SD
Age	34.5	10.2	35.1	10.5	33.9	9.8
Gender	1.2	0.4	1.1	0.3	1.3	0.5
Marital Status	2.1	0.8	2.0	0.7	2.2	0.9
Education	12.5	2.1	12.3	2.0	12.7	2.2
Income	15.2	3.5	14.8	3.2	15.6	3.8
Health Status	1.8	0.6	1.7	0.5	1.9	0.7
Employment	2.3	0.9	2.2	0.8	2.4	1.0
Family Size	3.2	1.5	3.1	1.4	3.3	1.6
Urban/Rural	1.1	0.3	1.0	0.2	1.2	0.4
Religion	1.5	0.5	1.4	0.4	1.6	0.6
Language	1.3	0.4	1.2	0.3	1.4	0.5
Migration	1.1	0.3	1.0	0.2	1.2	0.4
Health Insurance	1.2	0.4	1.1	0.3	1.3	0.5
Access to Services	1.4	0.5	1.3	0.4	1.5	0.6
Quality of Life	1.6	0.6	1.5	0.5	1.7	0.7
Life Satisfaction	1.8	0.7	1.7	0.6	1.9	0.8
Physical Health	1.5	0.5	1.4	0.4	1.6	0.6
Mental Health	1.3	0.4	1.2	0.3	1.4	0.5
Social Health	1.4	0.5	1.3	0.4	1.5	0.6
Overall Well-being	1.6	0.6	1.5	0.5	1.7	0.7

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-26-

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 35 40 45
 Cys Met Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu
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 Cys Asn Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala
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 Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg
 5 10 15
 att gaa gtg atc gta gat gat gat aac gtg atc act gat gcg ttt tct 152
 Ile Glu Val Ile Val Asp Asp Asp Asn Val Ile Thr Asp Ala Phe Ser
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 Ser Ser Thr Leu Phe Arg Gly Leu Glu Thr Ile Ile Lys Gly Arg Asp
 35 40 45 50
 cca cga gat gca ggc ttc atc gct caa agg att tgc ggg gta tgc act 248
 Pro Arg Asp Ala Gly Phe Ile Ala Gln Arg Ile Cys Gly Val Cys Thr
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 Tyr Ser His Tyr Lys Ala Gly Ile Thr Ala Val Glu Asn Ala Leu Gly
 70 75 80
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 Ile Thr Pro Pro Leu Asn Ala Gln Leu Val Arg Ser Leu Met Asn Met
 85 90 95

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ctt Leu 115	gat Asp	tgg Trp	tgc Cys	gat Asp	atc Ile 120	atg Met	agc Ser	gct Ala	tta Leu	aaa Lys 125	gcc Ala	gat Asp	ccc Pro	att Ile	caa Gln 130	440
gcg Ala	gca Ala	aaa Lys	ctt Leu	tct Ser 135	ttc Phe	aaa Lys	tac Tyr	agc Ser	cct Pro 140	tac Tyr	cct Pro	att Ile	aat Asn	acc Thr 145	ggg Gly	488
gcc Ala	ggt Gly	gaa Glu	tta Leu 150	aaa Lys	gcg Ala	gtt Val	caa Gln	aaa Lys 155	cgc Arg	ttg Leu	agc Ser	gat Asp	ttc Phe 160	gct Ala	aaa Lys	536
agc Ser	gga Gly	tct Ser 165	ttg Leu	ggg Gly	cct Pro	ttc Phe	agt Ser 170	aac Asn	ggc Gly	tat Tyr	tac Tyr	ggg Gly 175	cat His	aaa Lys	act Thr	584
tat Tyr 180	cgt Arg	tta Leu	agt Ser	ccg Pro	gag Glu	caa Gln 185	aat Asn	tta Leu	atc Ile	gtc Val 190	tta Leu	agc Ser	cac His	tac Tyr	ctc Leu	632
aag Lys 195	ctt Leu	tta Leu	gaa Glu	atc Ile	caa Gln 200	agg Arg	gaa Glu	gcg Ala	gcg Ala	aaa Lys 205	atg Met	acc Thr	gct Ala	att Ile	ttt Phe 210	680
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aag Lys	ttt Phe 245	gaa Glu	gtg Val	gtg Val	gcc Ala	aat Asn	ttc Phe 250	atc Ile	aac Asn	cat His	gct Ala	tac Tyr 255	tac Tyr	cct Pro	gat Asp	824
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ggc Gly 275	tgt Cys	ggc Gly	tta Leu	agg Arg	aat Asn 280	ttt Phe	atc Ile	gct Ala	tat Tyr	gaa Glu 285	gaa Glu	gtg Val	ctg Leu	ctt Leu	ggg Gly 290	920
agg Arg	gat Asp	aaa Lys	tac Tyr	ctt Leu 295	ttg Leu	agt Ser	agt Ser	ggg Gly	gtg Val 300	gtg Val	ctt Leu	gat Asp	ggg Gly	gat Asp 305	att Ile	968
tct Ser	aaa Lys	tta Leu	cac His 310	ccc Pro	att Ile	gat Asp	gaa Glu	agt Ser 315	ttg Leu	att Ile	aaa Lys	gaa Glu	gaa Glu 320	gtt Val	acg Thr	1016
cat His	tct Ser	tgg Trp 325	tat Tyr	caa Gln	tac Tyr	gaa Glu	gac Asp 330	act Thr	aaa Lys	gaa Glu	gtg Val 335	caa Gln	ctc Leu	cac His	cct Pro	1064

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565

570

575

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1837

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<212> PRT

<213> Helicobacter pylori

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His	Pro	Tyr	Asp	Gly	Gln	Thr	Asn	Pro	His	Tyr	Thr	Gly	Leu	Lys	Asp
		340						345					350		
Gly	Glu	Ser	Val	Gly	Ile	Glu	Asn	Lys	Ile	Ile	Pro	Ala	Lys	Val	Leu
		355					360					365			
Asp	Thr	Lys	Asn	Lys	Tyr	Ser	Trp	Ile	Lys	Ser	Pro	Arg	Tyr	Asp	Ser
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Lys	Pro	Met	Glu	Val	Gly	Pro	Leu	Ser	Ser	Val	Val	Val	Gly	Leu	Ala

[illegible]

<210> 21
 <211> 508
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 <213> Helicobacter pylori

<220>
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 <222> (51)...(455)

<400> 21

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                                     Met Gly
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aat ttg act tat tac gct tac atg tat ttg atc ctc ttt gta tgc ttg      104
Asn Leu Thr Tyr Tyr Ala Tyr Met Tyr Leu Ile Leu Phe Val Cys Leu
      5                                10                                15

ctg cct gtg tta tta atg ggg ctt gtt tgg agg ctt act cgc ccc ccc      152
Leu Pro Val Leu Leu Met Gly Leu Val Trp Arg Leu Thr Arg Pro Pro
      20                                25                                30

tta aag caa aat att cct aat aaa agc ctc tct tta gaa aat tta aac      200
Leu Lys Gln Asn Ile Pro Asn Lys Ser Leu Ser Leu Glu Asn Leu Asn
      35                                40                                50

gaa caa atc aaa aac ctt aaa agc gta cca gct tta gaa aaa ctg aaa      248
Glu Gln Ile Lys Asn Leu Lys Ser Val Pro Ala Leu Glu Lys Leu Lys
                        55                                60                                65

aac gac ttc aat gag cgt ttt aaa att tgc ccc aaa gat aaa gaa act      296
Asn Asp Phe Asn Glu Arg Phe Lys Ile Cys Pro Lys Asp Lys Glu Thr
                        70                                75                                80

ctg tgg tta gaa acg atc caa aaa tta gtc gct tca gaa ttt ttt gaa      344
Leu Trp Leu Glu Thr Ile Gln Lys Leu Val Ala Ser Glu Phe Phe Glu
                        85                                90                                95

tta gaa gac gct att aat ttt ggg caa gaa tta gaa aac gct aac cct      392
Leu Glu Asp Ala Ile Asn Phe Gly Gln Glu Leu Glu Asn Ala Asn Pro
      100                                105                                110

aat tac caa caa aaa atc gct aac gct acc ggc tta gcc ctt aag aat      440
Asn Tyr Gln Gln Lys Ile Ala Asn Ala Thr Gly Leu Ala Leu Lys Asn
      115                                120                                125                                130

aaa aaa gaa aaa gga tagaattgga ttttttagag attgtaggac aagtccttt      495
Lys Lys Glu Lys Gly
                        135

aaaaggagag gta      508
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<210> 22
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 <213> Helicobacter pylori

<400> 22

Met Gly Asn Leu Thr Tyr Tyr Ala Tyr Met Tyr Leu Ile Leu Phe Val

1	5	10	15
Cys Leu Leu Pro Val Leu Leu Met Gly Leu Val Trp Arg Leu Thr Arg			
20	25	30	
Pro Pro Leu Lys Gln Asn Ile Pro Asn Lys Ser Leu Ser Leu Glu Asn			
35	40	45	
Leu Asn Glu Gln Ile Lys Asn Leu Lys Ser Val Pro Ala Leu Glu Lys			
50	55	60	
Leu Lys Asn Asp Phe Asn Glu Arg Phe Lys Ile Cys Pro Lys Asp Lys			
65	70	75	80
Glu Thr Leu Trp Leu Glu Thr Ile Gln Lys Leu Val Ala Ser Glu Phe			
85	90	95	
Phe Glu Leu Glu Asp Ala Ile Asn Phe Gly Gln Glu Leu Glu Asn Ala			
100	105	110	
Asn Pro Asn Tyr Gln Gln Lys Ile Ala Asn Ala Thr Gly Leu Ala Leu			
115	120	125	
Lys Asn Lys Lys Glu Lys Gly			
130	135		

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<220>
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ttt tta gaa aaa gta tta gac aat caa gtt act gaa agt aaa gaa ttg	104
Phe Leu Glu Lys Val Leu Asp Asn Gln Val Thr Glu Ser Lys Glu Leu	
5	10
gtc agg ctt tat gat tat gat tta tac acg cta ggg gaa gta gcg gat	152
Val Arg Leu Tyr Asp Tyr Asp Leu Tyr Thr Leu Gly Glu Val Ala Asp	
20	25
cgc atg cgc caa aac atg cac caa aaa atc gtg tat ttt aat gtc aat	200
Arg Met Arg Gln Asn Met His Gln Lys Ile Val Tyr Phe Asn Val Asn	
35	40
agg cat tta aac cct agc aat att tgc gcg gac gct tgc aaa ttt tgc	248
Arg His Leu Asn Pro Ser Asn Ile Cys Ala Asp Ala Cys Lys Phe Cys	
55	60
gct ttt tca gcc cac aga aaa aac cca aac cct tat gaa atg agc tta	296
Ala Phe Ser Ala His Arg Lys Asn Pro Asn Pro Tyr Glu Met Ser Leu	
70	75
gaa gaa atc cta gaa aag gtt aaa aac tcc tac aac aag ggg att aaa	344
Glu Glu Ile Leu Glu Lys Val Lys Asn Ser Tyr Asn Lys Gly Ile Lys	
85	90
gaa gtc cat atc gtg agc gct cat aac cct aat tac tcc tat gaa tgg	392
Glu Val His Ile Val Ser Ala His Asn Pro Asn Tyr Ser Tyr Glu Trp	
100	105

tat tta aag gtg ttt gaa acc atc aag caa gaa atg cct aac ttg cat	440
Tyr Leu Lys Val Phe Glu Thr Ile Lys Gln Glu Met Pro Asn Leu His	
115 120 125 130	
tta aag gcc atg acc gct gca gaa gtg cat ttt tta agc gtt aaa ttc	488
Leu Lys Ala Met Thr Ala Ala Glu Val His Phe Leu Ser Val Lys Phe	
135 140 145	
aac aaa cct ttt gaa ttg gtg cta gaa gac atg ctc aaa gcc ggg gtg	536
Asn Lys Pro Phe Glu Leu Val Leu Glu Asp Met Leu Lys Ala Gly Val	
150 155 160	
gat tcc atg cct ggt ggg ggg gcg gag att ttt gat gaa gaa atc agg	584
Asp Ser Met Pro Gly Gly Gly Ala Glu Ile Phe Asp Glu Glu Ile Arg	
165 170 175	
cgt aaa atc tgt aat ggt aag gtg gga tct tct cgg tgg tta gaa atc	632
Arg Lys Ile Cys Asn Gly Lys Val Gly Ser Ser Arg Trp Leu Glu Ile	
180 185 190	
cat gct tat tgg cac aaa tta ggc aaa atg agt aac gct acc atg ctt	680
His Ala Tyr Trp His Lys Leu Gly Lys Met Ser Asn Ala Thr Met Leu	
195 200 205 210	
ttt ggg cat att gaa aat aaa atc cat cgc atc gat cac atg cta aga	728
Phe Gly His Ile Glu Asn Lys Ile His Arg Ile Asp His Met Leu Arg	
215 220 225	
atc aaa aaa atc caa agc cct aaa aat caa gta gaa aac aaa gaa ggg	776
Ile Lys Lys Ile Gln Ser Pro Lys Asn Gln Val Glu Asn Lys Glu Gly	
230 235 240	
ggg ttt aac gct ttt atc ccc ttg ttg tat caa aaa gaa aac aat tat	824
Gly Phe Asn Ala Phe Ile Pro Leu Leu Tyr Gln Lys Glu Asn Asn Tyr	
245 250 255	
ttg aat gtg gaa aaa tcc ccc agt gcg ata gaa atc tta aaa acc atc	872
Leu Asn Val Glu Lys Ser Pro Ser Ala Ile Glu Ile Leu Lys Thr Ile	
260 265 270	
gcc ata tct cgc att ctt tta aac aat atc cct cac att aaa gct tat	920
Ala Ile Ser Arg Ile Leu Leu Asn Asn Ile Pro His Ile Lys Ala Tyr	
275 280 285 290	
tgg gcg act ttg ggc ttg aat ttg gct tta gtg gct caa gaa ttt ggc	968
Trp Ala Thr Leu Gly Leu Asn Leu Ala Leu Val Ala Gln Glu Phe Gly	
295 300 305	
gct aac gat tta gac ggc acg ata gag ata gag agc att caa agc gcg	1016
Ala Asn Asp Leu Asp Gly Thr Ile Glu Ile Glu Ser Ile Gln Ser Ala	
310 315 320	
gca ggc gca aag agc cgg cat ggt tta gaa aaa gaa gat ttg ata ttt	1064
Ala Gly Ala Lys Ser Arg His Gly Leu Glu Lys Glu Asp Leu Ile Phe	
325 330 335	
aaa atc aag gac gct ggt ttt gtt gcg gta gaa agg gat agt ttg tat	1112
Lys Ile Lys Asp Ala Gly Phe Val Ala Val Glu Arg Asp Ser Leu Tyr	


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355                                360

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<211> 616
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(563)

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                                   1

aaa tta cct aaa aaa cga gtt tct aaa acc aaa tca caa aaa ctt atc      104
Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys Leu Ile
                    5                      10                      15

cat agc tta acc acc caa aaa aac aga gcc ttt ctc aaa aaa atc agc      152
His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys Ile Ser
                    20                      25                      30

gct aat gaa atg ctt tta gaa tta gaa aaa ggg gcg ttt aaa aaa aat      200
Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys Lys Asn
                    35                      40                      45                      50

gaa gct tat ttt att tct gat gaa gaa gat aaa aat tat gtt ttg gtg      248
Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val Leu Val
                    55                      60                      65

cca gat aac gtg atc tct ctt ttg gca gaa aac gcc aga aag gct ttt      296
Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys Ala Phe
                    70                      75                      80

gaa gcc agg ctt agg gcg gaa tta gaa agg gat att atc acc caa gcg      344
Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr Gln Ala
                    85                      90                      95

ccg att gat ttt gaa gac gtg cgc gaa gtt tcc ttg caa cta ttg gaa      392
Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu Leu Glu
                    100                      105                      110

aat tta cgc caa aaa gat ggg aat ttg cct aat atc aac acc tta aac      440
Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr Leu Asn
                    115                      120                      125                      130

ttt gtc aaa caa atc aaa aaa gaa cac cct aat tta ttc ttt aat ttt      488
Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe Asn Phe
                    135                      140                      145

gac aac atg ttc aaa caa ccc cct ttt aat gag aat aat ttt gaa aat      536
Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe Glu Asn
                    150                      155                      160

ttt gac aat agc gat gag gaa aat ttt taatgcaaac cattgatttt      583
Phe Asp Asn Ser Asp Glu Glu Asn Phe
                    165                      170

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gaaaaatttt cacaatatc caagcccggc cca

616

<210> 26
<211> 171
<212> PRT
<213> Helicobacter pylori

<400> 26
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20 25 30
Ile Ser Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys
35 40 45
Lys Asn Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val
50 55 60
Leu Val Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys
65 70 75 80
Ala Phe Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr
85 90 95
Gln Ala Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu
100 105 110
Leu Glu Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr
115 120 125
Leu Asn Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe
130 135 140
Asn Phe Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe
145 150 155 160
Glu Asn Phe Asp Asn Ser Asp Glu Glu Asn Phe
165 170

<210> 27
<211> 952
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(899)

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gaa aat att aat gaa aat att ttt gaa gaa gta ggg gac gct tgc gtt 104
Glu Asn Ile Asn Glu Asn Ile Phe Glu Glu Val Gly Asp Ala Cys Val
5 10 15
aaa tgc gct aag tgc gtg cca ggc tgc acc ata tac cgc att cat aaa 152
Lys Cys Ala Lys Cys Val Pro Gly Cys Thr Ile Tyr Arg Ile His Lys
20 25 30
gac gag gcg act tcg cct aga ggc ttt tta gat ttg atg cgc tta aac 200
Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg Leu Asn
35 40 45 50
gct caa aac aag ctc caa tta gac acg aat tta aaa cac ctt tta gaa 248

Ala	Gln	Asn	Lys	Leu	Gln	Leu	Asp	Thr	Asn	Leu	Lys	His	Leu	Leu	Glu		
				55					60					65			
act	tgc	ttt	tta	tgc	acc	gct	tgc	gtg	gaa	att	tgc	cct	ttt	cat	ttg		296
Thr	Cys	Phe	Leu	Cys	Thr	Ala	Cys	Val	Glu	Ile	Cys	Pro	Phe	His	Leu		
			70					75					80				
ccc	ata	gac	acc	tta	ata	gaa	aaa	gcc	aga	gaa	aaa	atc	gct	caa	aag		344
Pro	Ile	Asp	Thr	Leu	Ile	Glu	Lys	Ala	Arg	Glu	Lys	Ile	Ala	Gln	Lys		
		85					90					95					
cat	ggc	atc	gct	tgg	tat	aaa	aaa	tcc	tat	ttt	tcc	ctt	tta	aaa	aac		392
His	Gly	Ile	Ala	Trp	Tyr	Lys	Lys	Ser	Tyr	Phe	Ser	Leu	Leu	Lys	Asn		
	100					105					110						
cgc	aaa	aaa	atg	gat	agg	gtg	ttt	tca	act	gcg	cat	ttt	tta	gcc	cct		440
Arg	Lys	Lys	Met	Asp	Arg	Val	Phe	Ser	Thr	Ala	His	Phe	Leu	Ala	Pro		
115					120					125					130		
tgc	gtt	ttc	aag	caa	gta	ggg	gat	agt	tta	gag	cct	agg	gcg	gtg	ttt		488
Cys	Val	Phe	Lys	Gln	Val	Gly	Asp	Ser	Leu	Glu	Pro	Arg	Ala	Val	Phe		
				135					140					145			
aaa	ggt	ttg	ttc	aaa	cgc	ttt	aaa	aaa	agc	gcg	ctg	cct	cct	tta	aat		536
Lys	Gly	Leu	Phe	Lys	Arg	Phe	Lys	Lys	Ser	Ala	Leu	Pro	Pro	Leu	Asn		
			150					155					160				
caa	aaa	agt	ttt	tta	caa	aag	cat	gca	gaa	atg	aag	ctt	tta	gaa	aac		584
Gln	Lys	Ser	Phe	Leu	Gln	Lys	His	Ala	Glu	Met	Lys	Leu	Leu	Glu	Asn		
		165					170					175					
ccc	att	caa	aaa	gtg	gcc	att	ttt	ata	ggg	tgc	ttg	agc	aat	tac	cat		632
Pro	Ile	Gln	Lys	Val	Ala	Ile	Phe	Ile	Gly	Cys	Leu	Ser	Asn	Tyr	His		
	180					185					190						
tac	cag	caa	gtg	ggg	gaa	agc	ttg	ttg	tat	att	tta	gaa	aaa	ctc	aac		680
Tyr	Gln	Gln	Val	Gly	Glu	Ser	Leu	Leu	Tyr	Ile	Leu	Glu	Lys	Leu	Asn		
195					200				205					210			
att	caa	gcg	atc	atc	cct	aag	caa	gaa	tgc	tgc	tca	gcg	cct	gcg	tat		728
Ile	Gln	Ala	Ile	Ile	Pro	Lys	Gln	Glu	Cys	Cys	Ser	Ala	Pro	Ala	Tyr		
				215				220						225			
ttt	acc	ggc	gat	aaa	gac	acc	acg	ctt	ttt	tta	gtg	aaa	aaa	aac	ata		776
Phe	Thr	Gly	Asp	Lys	Asp	Thr	Thr	Leu	Phe	Leu	Val	Lys	Lys	Asn	Ile		
			230					235					240				
gaa	tgg	ttt	gaa	agc	tat	tta	gat	aaa	gtg	gat	gcg	atc	att	gtg	cct		824
Glu	Trp	Phe	Glu	Ser	Tyr	Leu	Asp	Lys	Val	Asp	Ala	Ile	Ile	Val	Pro		
		245					250					255					
gaa	gcc	aca	tgc	gct	aca	tgc	tca	tca	acg	att	att	aca	agg	tgt	ttt		872
Glu	Ala	Thr	Cys	Ala	Thr	Cys	Ser	Ser	Thr	Ile	Ile	Thr	Arg	Cys	Phe		
	260					265					270						
tgg	gcg	aaa	aag	ata	agg	att	tgt	atg	tga	agc	gctt	gg	aaaaaa	aatc			919
Trp	Ala	Lys	Lys	Ile	Arg	Ile	Cys	Met									
275					280												

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952

<210> 28
<211> 283
<212> PRT
<213> Helicobacter pylori

<400> 28
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20 25 30
His Lys Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg
35 40 45
Leu Asn Ala Gln Asn Lys Leu Gln Leu Asp Thr Asn Leu Lys His Leu
50 55 60
Leu Glu Thr Cys Phe Leu Cys Thr Ala Cys Val Glu Ile Cys Pro Phe
65 70 75 80
His Leu Pro Ile Asp Thr Leu Ile Glu Lys Ala Arg Glu Lys Ile Ala
85 90 95
Gln Lys His Gly Ile Ala Trp Tyr Lys Lys Ser Tyr Phe Ser Leu Leu
100 105 110
Lys Asn Arg Lys Lys Met Asp Arg Val Phe Ser Thr Ala His Phe Leu
115 120 125
Ala Pro Cys Val Phe Lys Gln Val Gly Asp Ser Leu Glu Pro Arg Ala
130 135 140
Val Phe Lys Gly Leu Phe Lys Arg Phe Lys Lys Ser Ala Leu Pro Pro
145 150 155 160
Leu Asn Gln Lys Ser Phe Leu Gln Lys His Ala Glu Met Lys Leu Leu
165 170 175
Glu Asn Pro Ile Gln Lys Val Ala Ile Phe Ile Gly Cys Leu Ser Asn
180 185 190
Tyr His Tyr Gln Gln Val Gly Glu Ser Leu Leu Tyr Ile Leu Glu Lys
195 200 205
Leu Asn Ile Gln Ala Ile Ile Pro Lys Gln Glu Cys Cys Ser Ala Pro
210 215 220
Ala Tyr Phe Thr Gly Asp Lys Asp Thr Thr Leu Phe Leu Val Lys Lys
225 230 235 240
Asn Ile Glu Trp Phe Glu Ser Tyr Leu Asp Lys Val Asp Ala Ile Ile
245 250 255
Val Pro Glu Ala Thr Cys Ala Thr Cys Ser Ser Thr Ile Ile Thr Arg
260 265 270
Cys Phe Trp Ala Lys Lys Ile Arg Ile Cys Met
275 280

<210> 29
<211> 1361
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (49)...(1305)

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Met Lys Glu
1

57

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Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp Ile Arg Lys	
5 10 15	
aca caa aat gcg cga tgg ata gat caa aaa tgc acc cct gat gtg ttg	153
Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro Asp Val Leu	
20 25 30 35	
tct ctt gtt gct gat tgt att tta gag ttt acg caa tgt aat att gga	201
Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys Asn Ile Gly	
40 45 50	
aaa tca ttt tct att agg gat att tgg gat agc cct tac acc aat gaa	249
Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr Thr Asn Glu	
55 60 65	
aat gtt aaa atg att ttt tct aaa cct gat tta aat tct gac ttt tcc	297
Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser Asp Phe Ser	
70 75 80	
atg cat gaa tac gat aag ttt ttt tct cag cct att aaa tta tta gcc	345
Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys Leu Leu Ala	
85 90 95	
tat agc ggt att tta ttt gaa aca aaa act ggc aat aga aat att tat	393
Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg Asn Ile Tyr	
100 105 110 115	
acc ata caa aac ata gag cta tta gaa tat ctc atg caa aga gaa aca	441
Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln Arg Glu Thr	
120 125 130	
aac gct ttg aaa ttc ctt att tta tat att caa aag gta tta atg gat	489
Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val Leu Met Asp	
135 140 145	
agt ggg att tat cct tta ttt gac aac ttt tta caa aaa caa gac aca	537
Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys Gln Asp Thr	
150 155 160	
gaa agt ttt aag caa cta aaa gat ggt ttc act cat ttt act atc aat	585
Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe Thr Ile Asn	
165 170 175	
aac aca gca atc aat aac gct acg gaa tgt ttt agg att ttt act aaa	633
Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile Phe Thr Lys	
180 185 190 195	
att atc aat cct tta gct ttt tat tat ggt aaa aaa ggc aca aga aaa	681
Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly Thr Arg Lys	
200 205 210	
ggg tat ttg tcc aac act ata att aca aaa gat gag ctt aat tat aat	729
Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu Asn Tyr Asn	
215 220 225	
cgt atc aat tgg cga gat ata gga aaa gat aaa aat acc acc aga caa	777
Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr Thr Arg Gln	
230 235 240	

gaa tac gat ctt ata aac tct aaa agg att gct aat tct aac tat ctt Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser Asn Tyr Leu 245 250 255																825
att tca aaa gct aag aaa gtg gtg aaa cga tat aat gat aga ttt aat Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn 260 265 270 275																873
aat tct ctc tct gaa gta aaa caa gaa aaa gaa gag tcg caa gcc aca Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr 280 285 290																921
caa ata cac cat att ttt ccc atc caa gac ttt ccc att att gct aac Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile Ile Ala Asn 295 300 305																969
tat ata gag aat ctt atc gca ctc act cct aat caa cat ttt att tac Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His Phe Ile Tyr 310 315 320																1017
gcc cac cct aat aat caa acc cgc ttg att gat aaa gat ttt caa tat Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr 325 330 335																1065
atc tgc tta tta gct aaa acg acc aca att ctt aat gac act caa ggc Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly 340 345 350 355																1113
gta tat gat tgg aat gat tat att gtt gtg ttg aat atg ggc ctc aaa Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met Gly Leu Lys 360 365 370																1161
aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val 375 380 385																1209
ata gat gct ttt tat ttt gat ttt aac aag agc aaa gat cca agt tgg Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp 390 395 400																1257
tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe 405 410 415																1305
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<210> 30
<211> 419
<212> PRT
<213> Helicobacter pylori
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Met	Lys	Glu	Gln	Ser	Met	Ile	Asp	Phe	Leu	Lys	Leu	Arg	Asp	Tyr	Asp
1				5					10					15	
Ile	Arg	Lys	Thr	Gln	Asn	Ala	Arg	Trp	Ile	Asp	Gln	Lys	Cys	Thr	Pro
			20					25					30		
Asp	Val	Leu	Ser	Leu	Val	Ala	Asp	Cys	Ile	Leu	Glu	Phe	Thr	Gln	Cys
		35				40						45			

Asn	Ile	Gly	Lys	Ser	Phe	Ser	Ile	Arg	Asp	Ile	Trp	Asp	Ser	Pro	Tyr
50						55					60				
Thr	Asn	Glu	Asn	Val	Lys	Met	Ile	Phe	Ser	Lys	Pro	Asp	Leu	Asn	Ser
65					70					75					80
Asp	Phe	Ser	Met	His	Glu	Tyr	Asp	Lys	Phe	Phe	Ser	Gln	Pro	Ile	Lys
				85					90					95	
Leu	Leu	Ala	Tyr	Ser	Gly	Ile	Leu	Phe	Glu	Thr	Lys	Thr	Gly	Asn	Arg
			100					105					110		
Asn	Ile	Tyr	Thr	Ile	Gln	Asn	Ile	Glu	Leu	Leu	Glu	Tyr	Leu	Met	Gln
		115					120					125			
Arg	Glu	Thr	Asn	Ala	Leu	Lys	Phe	Leu	Ile	Leu	Tyr	Ile	Gln	Lys	Val
	130					135					140				
Leu	Met	Asp	Ser	Gly	Ile	Tyr	Pro	Leu	Phe	Asp	Asn	Phe	Leu	Gln	Lys
145					150					155					160
Gln	Asp	Thr	Glu	Ser	Phe	Lys	Gln	Leu	Lys	Asp	Gly	Phe	Thr	His	Phe
				165					170					175	
Thr	Ile	Asn	Asn	Thr	Ala	Ile	Asn	Asn	Ala	Thr	Glu	Cys	Phe	Arg	Ile
			180					185					190		
Phe	Thr	Lys	Ile	Ile	Asn	Pro	Leu	Ala	Phe	Tyr	Tyr	Gly	Lys	Lys	Gly
		195					200					205			
Thr	Arg	Lys	Gly	Tyr	Leu	Ser	Asn	Thr	Ile	Ile	Thr	Lys	Asp	Glu	Leu
	210					215					220				
Asn	Tyr	Asn	Arg	Ile	Asn	Trp	Arg	Asp	Ile	Gly	Lys	Asp	Lys	Asn	Thr
225					230					235					240
Thr	Arg	Gln	Glu	Tyr	Asp	Leu	Ile	Asn	Ser	Lys	Arg	Ile	Ala	Asn	Ser
				245					250					255	
Asn	Tyr	Leu	Ile	Ser	Lys	Ala	Lys	Lys	Val	Val	Lys	Arg	Tyr	Asn	Asp
			260					265					270		
Arg	Phe	Asn	Asn	Ser	Leu	Ser	Glu	Val	Lys	Gln	Glu	Lys	Glu	Glu	Ser
		275					280					285			
Gln	Ala	Thr	Gln	Ile	His	His	Ile	Phe	Pro	Ile	Gln	Asp	Phe	Pro	Ile
	290					295					300				
Ile	Ala	Asn	Tyr	Ile	Glu	Asn	Leu	Ile	Ala	Leu	Thr	Pro	Asn	Gln	His
305					310					315					320
Phe	Ile	Tyr	Ala	His	Pro	Asn	Asn	Gln	Thr	Arg	Leu	Ile	Asp	Lys	Asp
				325					330					335	
Phe	Gln	Tyr	Ile	Cys	Leu	Leu	Ala	Lys	Thr	Thr	Thr	Ile	Leu	Asn	Asp
			340					345					350		
Thr	Gln	Gly	Val	Tyr	Asp	Trp	Asn	Asp	Tyr	Ile	Val	Val	Leu	Asn	Met
		355					360					365			
Gly	Leu	Lys	Thr	Thr	Ile	Phe	Ser	Gln	Val	Lys	Asn	Glu	Trp	Glu	Leu
	370					375					380				
Leu	Lys	Val	Ile	Asp	Ala	Phe	Tyr	Phe	Asp	Phe	Asn	Lys	Ser	Lys	Asp
385					390					395					400
Pro	Ser	Trp	Ser	Tyr	Leu	Leu	Asp	Lys	Asn	Asp	Leu	Arg	Ala	Phe	Lys
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Leu	Lys	Phe													

<210> 31
 <211> 763
 <212> DNA
 <213> Helicobacter pylori

 <220>
 <221> CDS
 <222> (53)...(709)

 <400> 31

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Phe Ala Met Ile Gly Ser Gly Gly Phe Ile Ala Pro Lys His Leu Gln	
5 10 15	
gcg att aga gat aca ggg cat ttt ttg gat tgc tct ttt gat att cat	154
Ala Ile Arg Asp Thr Gly His Phe Leu Asp Cys Ser Phe Asp Ile His	
20 25 30	
gat agc gtg ggg gtt tta gat gag tat ttc gcg caa tca gag ttt ttt	202
Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu Phe Phe	
35 40 45 50	
acg aat att gaa gat ttt gaa aag cat tta gag caa tct aag gat atg	250
Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys Asp Met	
55 60 65	
ggg aaa gaa atc aac tat ttg agt gtt tgc acg cct acg cac acg cat	298
Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His Thr His	
70 75 80	
ttt gat cac atc cgt ttc ggg tta aga aac ggc atg cat gtg att tgt	346
Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val Ile Cys	
85 90 95	
gaa aaa ccc tta gtt tta gac cct ggc gaa ata caa gaa ttg aaa gat	394
Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu Lys Asp	
100 105 110	
tta gag gtg aaa cac caa aaa agg gtg ttt agt ctt tta ccc ttg cgc	442
Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro Leu Arg	
115 120 125 130	
ttg cat tgc gac acg ctg gct ttg aaa gaa aaa att aag agc gaa tta	490
Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser Glu Leu	
135 140 145	
gac aaa aac cct agc aag gtg ttt gac atc acg ctc act tat atc agc	538
Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr Ile Ser	
150 155 160	
gtt caa ggg aaa tgg tat ttt tct tca tgg cga gcg gat gtg aat agg	586
Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val Asn Arg	
165 170 175	
agc gga ggg tta gcc act caa atg ggg gtg aat att ttt gac act tta	634
Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp Thr Leu	
180 185 190	
atc tat ttg ttt gga agc gtt aaa gac aag gtt atc aat aaa gaa gag	682
Ile Tyr Leu Phe Gly Ser Val Lys Asp Lys Val Ile Asn Lys Glu Glu	
195 200 205 210	
cct gat tgc gta ggg gga tac tct ttt tagagcatgc caaaataaga	729
Pro Asp Cys Val Gly Gly Tyr Ser Phe	
215	

tggttttttt ccatcaatcc agaacacatg ggag

763

<210> 32
 <211> 219
 <212> PRT
 <213> Helicobacter pylori

<400> 32

Met Leu Phe Ala Met Ile Gly Ser Gly Gly Phe Ile Ala Pro Lys His
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 Leu Gln Ala Ile Arg Asp Thr Gly His Phe Leu Asp Cys Ser Phe Asp
 20 25 30
 Ile His Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu
 35 40 45
 Phe Phe Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys
 50 55 60
 Asp Met Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His
 65 70 75 80
 Thr His Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val
 85 90 95
 Ile Cys Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu
 100 105 110
 Lys Asp Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro
 115 120 125
 Leu Arg Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser
 130 135 140
 Glu Leu Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr
 145 150 155 160
 Ile Ser Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val
 165 170 175
 Asn Arg Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp
 180 185 190
 Thr Leu Ile Tyr Leu Phe Gly Ser Val Lys Asp Lys Val Ile Asn Lys
 195 200 205
 Glu Glu Pro Asp Cys Val Gly Gly Tyr Ser Phe
 210 215

<210> 33
 <211> 1465
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1412)

<400> 33

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 Met Phe
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 Leu Leu Arg His Leu Thr Ser Ala Cys Val Phe Leu Ala Ser Lys Cys
 5 10 15
 ttg ccg gac tcc ttt gtc ttg gtc gct ctt tta tgc ttt gtc gtg ttt 152
 Leu Pro Asp Ser Phe Val Leu Val Ala Leu Leu Ser Phe Val Val Phe
 20 25 30

gtt Val 35	ctt Leu	gtt Val	tat Tyr	tgc Cys	ttg Leu 40	aca Thr	ggg Gly	caa Gln	gac Asp	gct Ala 45	ttt Phe	tct Ser	gtc Val	att Ile	tct Ser 50	200
agt Ser	tgg Trp	ggg Gly	aat Asn	ggc Gly 55	gct Ala	tgg Trp	acg Thr	ctt Leu	tta Leu 60	ggg Gly	ttt Phe	tct Ser	atg Met	caa Gln 65	atg Met	248
gcc Ala	ctt Leu	att Ile	ttg Leu 70	gtg Val	ttg Leu	ggg Gly	cag Gln	gct Ala 75	ctg Leu	gct Ala	aac Asn	gct Ala	aaa Lys 80	tta Leu	gtc Val	296
caa Gln	aag Lys	ctt Leu 85	tta Leu	aaa Lys	tat Tyr	cta Leu	gcg Ala 90	tct Ser	tta Leu	cct Pro	aaa Lys	ggg Gly 95	tat Tyr	tat Tyr	acg Thr	344
gct Ala 100	tta Leu	tgg Trp	ttg Leu	gtt Val	act Thr	ttt Phe 105	tta Leu	tcg Ser	tta Leu	atc Ile	gct Ala 110	aat Asn	tgg Trp	atc Ile	aac Asn	392
tgg Trp 115	ggg Gly	ttt Phe	ggc Gly	ttg Leu	gtg Val 120	att Ile	agt Ser	gcg Ala	att Ile	ttt Phe 125	gca Ala	aaa Lys	gag Glu	atc Ile	gcc Ala 130	440
aaa Lys	aat Asn	gtt Val	aag Lys	ggg Gly 135	gtg Val	gat Asp	tac Tyr	agg Arg	ctg Leu 140	ctc Leu	att Ile	gct Ala	agc Ser	gct Ala 145	tat Tyr	488
tcg Ser	ggg Gly	ttt Phe 150	gtc Val	atc Ile	tgg Trp	cat His	ggg Gly 155	ggg Gly	tta Leu	tca Ser	ggc Gly	tct Ser	atc Ile 160	cct Pro	tta Leu	536
agc Ser	gtt Val	gcc Ala 165	acc Thr	caa Gln	aat Asn	gaa Glu	aat Asn	cta Leu	tcc Ser	aaa Lys	ata Ile	agc Ser 175	gct Ala	ggg Gly	gtg Val	584
att Ile 180	gaa Glu	aaa Lys	gct Ala	atc Ile	cct Pro	atc Ile 185	agt Ser	cag Gln	acg Thr	att Ile	ttt Phe 190	tct Ser	tct Ser	tat Tyr	aat Asn	632
tta Leu 195	atc Ile	att Ile	ata Ile	ggg Gly	atc Ile 200	att Ile	ctt Leu	gta Val	ggg Gly	tta Leu 205	ccc Pro	ttt Phe	tta Leu	atg Met	gca Ala 210	680
atg Met	atc Ile	cac His	cct Pro	aaa Lys 215	aaa Lys	gaa Glu	gaa Glu	atc Ile	gtt Val 220	gag Glu	att Ile	gat Asp	tca Ser	aag Lys 225	ctt Leu	728
tta Leu	aaa Lys	gac Asp	gag Glu 230	tac Tyr	aaa Lys	gag Glu	att Ile	gaa Glu 235	ctc Leu	att Ile	agc Ser	cac His	caa Gln 240	caa Gln	gac Asp	776
aaa Lys	acg Thr	atc Ile 245	gcg Ala	cat His	ttt Phe	ttg Leu	gaa Glu 250	aac Asn	agc Ser	gct Ala	ttg Leu	ctt Leu 255	tct Ser	tat Tyr	ctt Leu	824
ttg Leu	gtt Val	ttt Phe	ttg Leu	ggg Gly	ttt Phe	ggg Gly	tat Tyr	ctt Leu	ggg Gly	gtt Val	tat Tyr	ttt Phe	ttt Phe	aaa Lys	ggg Gly	872

[illegible]

[illegible]

-48-

<211> 1114
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1061)

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tgg atg gtg gtt att ggg gct tta att tgc atg ctt tta ggg gtg ttt      104
Trp Met Val Val Ile Gly Ala Leu Ile Cys Met Leu Leu Gly Val Phe
      5                      10                      15

atc ttc ttc act agc atg tcg gtt aaa aaa ttt tta agc gct tat ctt      152
Ile Phe Phe Thr Ser Met Ser Val Lys Lys Phe Leu Ser Ala Tyr Leu
      20                      25                      30

aac gct tat ttg gat caa cgc ccc cat att aag ggc atg ggg att gca      200
Asn Ala Tyr Leu Asp Gln Arg Pro His Ile Lys Gly Met Gly Ile Ala
      35                      40                      45                      50

ggc act ccc ttt gaa tgc gaa ggg ttt ttt aaa atc gca tgc gtt tct      248
Gly Thr Pro Phe Glu Cys Glu Gly Phe Phe Lys Ile Ala Cys Val Ser
      55                      60                      65

aaa gag ctc agt ttt tta gac tct caa aac tcc cct att gtg aat ttt      296
Lys Glu Leu Ser Phe Leu Asp Ser Gln Asn Ser Pro Ile Val Asn Phe
      70                      75                      80

aaa aat ttg agt att aag ctc cgt tct tta gat aaa agc tct ctt act      344
Lys Asn Leu Ser Ile Lys Leu Arg Ser Leu Asp Lys Ser Ser Leu Thr
      85                      90                      95

ctt tct gtc cat tct caa atc aaa tcc cct att tta gaa caa gat atg      392
Leu Ser Val His Ser Gln Ile Lys Ser Pro Ile Leu Glu Gln Asp Met
      100                      105                      110

cag caa aaa atc agc caa atc ccc cta aaa gac ttg aat gcc tta tta      440
Gln Gln Lys Ile Ser Gln Ile Pro Leu Lys Asp Leu Asn Ala Leu Leu
      115                      120                      125                      130

gaa aaa atg aaa ccc acg cgc ttg aat tgc tct tta aca ttc aac gct      488
Glu Lys Met Lys Pro Thr Arg Leu Asn Cys Ser Leu Thr Phe Asn Ala
      135                      140                      145

cta gat gaa aaa acc tta aac gac aac tta aaa tgc gat ttg act aat      536
Leu Asp Glu Lys Thr Leu Asn Asp Asn Leu Lys Cys Asp Leu Thr Asn
      150                      155                      160

gcg gaa aat atc ctt gct tac act ttt ttt caa gag ggt tta atg gag      584
Ala Glu Asn Ile Leu Ala Tyr Thr Phe Phe Gln Glu Gly Leu Met Glu
      165                      170                      175

gct caa gaa aat cta tcc ctt aaa aat att ttt aaa acc ttg agt tct      632
Ala Gln Glu Asn Leu Ser Leu Lys Asn Ile Phe Lys Thr Leu Ser Ser

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180			185			190													
aaa Lys 195	gac Asp	gct Ala	aaa Lys	gcc Ala	ata Ile 200	gaa Glu	gag Glu	ttg Leu	caa Gln	gac Asp 205	aaa Lys	ctg Leu	cgt Arg	ttt Phe	tca Ser 210				680
gcg Ala	cca Pro	aag Lys	ttg Leu	ggc Gly 215	gtt Val	tct Ser	atc Ile	caa Gln	gcg Ala 220	cac His	cat His	ctt Leu	aaa Lys	aac Asn 225	ctt Leu				728
ttg Leu	gaa Glu	gcc Ala	ttt Phe 230	tat Tyr	cac His	caa Gln	aat Asn	aaa Lys 235	gag Glu	agt Ser	ttg Leu	ggc Gly	ttt Phe 240	ttt Phe	tcc Ser				776
cct Pro	tat Tyr	ttt Phe 245	agt Ser	ttg Leu	cga Arg	tct Ser	caa Gln 250	acc Thr	cct Pro	agc Ser	gtc Val	tct Ser 255	tat Tyr	gaa Glu	agc Ser				824
gcg Ala 260	tta Leu	gct Ala	tct Ser	tta Leu	gaa Glu 265	aac Asn	tat Tyr	ttt Phe	atg Met	gct Ala 270	ttg Leu	ttc Phe	caa Gln	tcc Ser	cat His				872
ttt Phe 275	aaa Lys	gac Asp	gat Asp	acc Thr	gca Ala 280	ctc Leu	caa Gln	cag Gln	aat Asn	ttt Phe 285	aaa Lys	gga Gly	ttg Leu	ttg Leu	caa Gln 290				920
gcc Ala	ttt Phe	gtt Val	tct Ser	atg Met 295	gct Ala	aaa Lys	gac Asp	aaa Lys	cga Arg 300	tcc Ser	caa Gln	atc Ile	gct Ala	ctt Leu 305	aac Asn				968
gcc Ala	caa Gln	gct Ala	aaa Lys 310	gac Asp	aac Asn	gcc Ala	aag Lys	cta Leu 315	act Thr	ttt Phe	aac Asn	gcc Ala	ttg Leu 320	tta Leu	gaa Glu				1016
agc Ser	ctt Leu	agc Ser 325	gtg Val	aat Asn	ttc Phe	ttt Phe	caa Gln 330	tct Ser	tac Tyr	aaa Lys	ata Ile	agc Ser 335	cat His	gag Glu				1061	
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<210> 36
<211> 337
<212> PRT
<213> Helicobacter pylori
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Val	Phe	Ile	Phe	Phe	Thr	Ser	Met	Ser	Val	Lys	Lys	Phe	Leu	Ser	Ala	
			20					25					30			
Tyr	Leu	Asn	Ala	Tyr	Leu	Asp	Gln	Arg	Pro	His	Ile	Lys	Gly	Met	Gly	
		35					40					45				
Ile	Ala	Gly	Thr	Pro	Phe	Glu	Cys	Glu	Gly	Phe	Phe	Lys	Ile	Ala	Cys	
	50					55					60					
Val	Ser	Lys	Glu	Leu	Ser	Phe	Leu	Asp	Ser	Gln	Asn	Ser	Pro	Ile	Val	
65					70					75				80		
Asn	Phe	Lys	Asn	Leu	Ser	Ile	Lys	Leu	Arg	Ser	Leu	Asp	Lys	Ser	Ser	
			85						90					95		
Leu	Thr	Leu	Ser	Val	His	Ser	Gln	Ile	Lys	Ser	Pro	Ile	Leu	Glu	Gln	

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<220>
<221> CDS
<222> (52) ... (165)
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-52-

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100105110																
cta Leu	agc Ser	gtg Val	gcg Ala	act Thr	tta Leu	att Ile	gtg Val	ctt Leu	ttt Phe	tgc Cys	aaa Lys	att Ile	aac Asn	gct Ala	aat Asn	440
115120125130																
gaa Glu	atc Ile	gct Ala	cat His	tca Ser	agc Ser	gtg Val	ttt Phe	aaa Lys	tcc Ser	ggc Gly	atg Met	caa Gln	gcg Ala	tgc Cys	gtg Val	488
135140145																
tgc Cys	gtg Val	ttg Leu	ggc Gly	gtg Val	gcg Ala	tgg Trp	ttg Leu	ggc Gly	gat Asp	act Thr	ttt Phe	gtg Val	agc Ser	aat Asn	cat His	536
150155160																
ata Ile	gat Asp	gag Glu	atc Ile	aaa Lys	cga Arg	tac Tyr	gct Ala	tct Ser	ttt Phe	ttg Leu	atc Ile	gca Ala	gat Asp	tat Tyr	ccg Pro	584
165170175																
ttt Phe	tta Leu	tta Leu	gcc Ala	gta Val	gcg Ala	ctc Leu	ttt Phe	ttg Leu	gct Ala	tcc Ser	atg Met	ctt Leu	ttg Leu	tat Tyr	tcg Ser	632
180185190																
caa Gln	gcc Ala	gcc Ala	acc Thr	tct Ser	aaa Lys	gcg Ala	ctc Leu	atc Ile	cca Pro	agc Ser	gtg Val	atc Ile	aca Thr	gcc Ala	tta Leu	680
195200205210																
ggc Gly	att Ile	agc Ser	gct Ala	aat Asn	cat His	acg Thr	gag Glu	cat His	ttg Leu	tat Tyr	att Ile	atc Ile	gtg Val	gct Ala	tcg Ser	728
215220225																
ttt Phe	gcg Ala	agc Ser	gtt Val	tcg Ser	gcg Ala	ttg Leu	ttt Phe	gtg Val	tta Leu	ccc Pro	act Thr	tac Tyr	ccc Pro	act Thr	tta Leu	776
230235240																
cta Leu	gga Gly	gcg Ala	atc Ile	gct Ala	atg Met	gat Asp	aac Asn	acc Thr	ggc Gly	acc Thr	act Thr	aaa Lys	atg Met	ggc Gly	cgt Arg	824
245250255																
tat Tyr	gtg Val	ttt Phe	gat Asp	cat His	gcg Ala	ttt Phe	ttg Leu	atc Ile	cct Pro	ggg Gly	gtt Val	tta Leu	gtc Val	gtg Val	tct Ser	872
260265270																
ttg Leu	agc Ser	gta Val	gcg Ala	tta Leu	ggg Gly	ttt Phe	gtt Val	gtc Val	gcg Ala	ccg Pro	tta Leu	gtt Val	ttg Leu			914
275280285																
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<210> 42
<211> 288
<212> PRT
<213> Helicobacter pylori
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 Ile Met Gly Phe Thr Asp Leu Lys Leu Asp Ser Asp Pro His Tyr Leu
 35 40 45
 Glu Arg Leu Lys Ala Gly Lys Ile Ser Pro Pro Lys Ile Lys Glu Glu
 50 55 60
 Lys Glu Thr Ser Lys Asn Ala Lys Leu Ser Leu Trp Ile Phe Ile Gly
 65 70 75 80
 Gly Val Val Ala Ile Val Phe Tyr Ala Ser Ala Ile Ser Lys Asn Ile
 85 90 95
 Ala Phe Val Ser Pro Val Val Leu Gly Arg Asp His Ala Ile Val Ser
 100 105 110
 Phe Met Leu Ser Val Ala Thr Leu Ile Val Leu Phe Cys Lys Ile Asn
 115 120 125
 Ala Asn Glu Ile Ala His Ser Ser Val Phe Lys Ser Gly Met Gln Ala
 130 135 140
 Cys Val Cys Val Leu Gly Val Ala Trp Leu Gly Asp Thr Phe Val Ser
 145 150 155 160
 Asn His Ile Asp Glu Ile Lys Arg Tyr Ala Ser Phe Leu Ile Ala Asp
 165 170 175
 Tyr Pro Phe Leu Leu Ala Val Ala Leu Phe Leu Ala Ser Met Leu Leu
 180 185 190
 Tyr Ser Gln Ala Ala Thr Ser Lys Ala Leu Ile Pro Ser Val Ile Thr
 195 200 205
 Ala Leu Gly Ile Ser Ala Asn His Thr Glu His Leu Tyr Ile Ile Val
 210 215 220
 Ala Ser Phe Ala Ser Val Ser Ala Leu Phe Val Leu Pro Thr Tyr Pro
 225 230 235 240
 Thr Leu Leu Gly Ala Ile Ala Met Asp Asn Thr Gly Thr Thr Lys Met
 245 250 255
 Gly Arg Tyr Val Phe Asp His Ala Phe Leu Ile Pro Gly Val Leu Val
 260 265 270
 Val Ser Leu Ser Val Ala Leu Gly Phe Val Val Ala Pro Leu Val Leu
 275 280 285

<210> 43
 <211> 1237
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (51)...(1184)

<400> 43

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 Glu Asn Ser Ser Ile Trp Ser Asn Pro Ala Phe Val Ala Ile Ile Cys
 5 10 15
 atg tgc gtt ctt agc ctt tta agg ctc aat gtc atg ctt tct atg att 152
 Met Cys Val Leu Ser Leu Arg Leu Asn Val Met Leu Ser Met Ile
 20 25 30
 agt gcg act ctc ata gca gga ctt atg gga ggg ctt ggg atc acg gag 200
 Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile Thr Glu

35	40										45					50					
agt ttt aat gca atg ata gac ggc atg aaa ggc aat ttg aac atc gct	248																				
Ser Phe Asn Ala Met Ile Asp Gly Met Lys Gly Asn Leu Asn Ile Ala																					
556065																					
tta agc tac atc ctt tta ggg gct tta gcg gta gcg atc gct aaa agc	296																				
Leu Ser Tyr Ile Leu Leu Gly Ala Leu Ala Val Ala Ile Ala Lys Ser																					
707580																					
aat ctc att aaa gtc gct ttg agt aaa tta ata ggt tta atg gat tac	344																				
Asn Leu Ile Lys Val Ala Leu Ser Lys Leu Ile Gly Leu Met Asp Tyr																					
859095																					
aag cga tcc act ttt tgc ttt ttg atc gct ttc atc gca tgc ttt tcg	392																				
Lys Arg Ser Thr Phe Cys Phe Leu Ile Ala Phe Ile Ala Cys Phe Ser																					
100105110																					
caa aat tta gtg ccg gtg cat atc gct ttt atc cct att tta atc ccc	440																				
Gln Asn Leu Val Pro Val His Ile Ala Phe Ile Pro Ile Leu Ile Pro																					
115120125130																					
cct ctt ttg cat tta atg aac cgg cta gaa ttg gat aga aga gcg gtc	488																				
Pro Leu Leu His Leu Met Asn Arg Leu Glu Leu Asp Arg Arg Ala Val																					
135140145																					
gct tgc gct tta acc ttt ggc ttg caa gcc ccc tac ttg gtg ctt cct	536																				
Ala Cys Ala Leu Thr Phe Gly Leu Gln Ala Pro Tyr Leu Val Leu Pro																					
150155160																					
gta ggg ttt ggc ttg att ttt caa acc acc att tta gag caa tta aaa	584																				
Val Gly Phe Gly Leu Ile Phe Gln Thr Thr Ile Leu Glu Gln Leu Lys																					
165170175																					
gct aat ggc gtt agc acc acc ata gcg caa atc aca gga gtg atg tgg	632																				
Ala Asn Gly Val Ser Thr Thr Ile Ala Gln Ile Thr Gly Val Met Trp																					
180185190																					
ata gcg ggg tta gcg atg gtc gtt gga ctg ctt gtt gct gta tta acg	680																				
Ile Ala Gly Leu Ala Met Val Val Gly Leu Leu Val Ala Val Leu Thr																					
195200205210																					
cta tac aaa aaa ccc agg cac tac aaa gag aaa tct ttt aat ata gaa	728																				
Leu Tyr Lys Lys Pro Arg His Tyr Lys Glu Lys Ser Phe Asn Ile Glu																					
215220225																					
aat tac gcc tcg ctt caa tta aac tac cat gac tac ttg act ttt ata	776																				
Asn Tyr Ala Ser Leu Gln Leu Asn Tyr His Asp Tyr Leu Thr Phe Ile																					
230235240																					
ggg att gtc gta gcg ttt gtg atc caa tta gcc acc gat tcg atg ccc	824																				
Gly Ile Val Val Ala Phe Val Ile Gln Leu Ala Thr Asp Ser Met Pro																					
245250255																					
tta gcc gcc ttt tta gcg tta gcg atc atc tta tta ggc cgt ggc att	872																				
Leu Ala Ala Phe Leu Ala Leu Ala Ile Ile Leu Leu Gly Arg Gly Ile																					
260265270																					
aag ttt aaa gaa aca gac tcg ctt atg gat gat agc gtg aaa atg atg	920																				

Met Trp Ile Ala Gly Leu Ala Met Val Val Gly Leu Leu Val Ala Val
 195 200 205
 Leu Thr Leu Tyr Lys Lys Pro Arg His Tyr Lys Glu Lys Ser Phe Asn
 210 215 220
 Ile Glu Asn Tyr Ala Ser Leu Gln Leu Asn Tyr His Asp Tyr Leu Thr
 225 230 235 240
 Phe Ile Gly Ile Val Val Ala Phe Val Ile Gln Leu Ala Thr Asp Ser
 245 250 255
 Met Pro Leu Ala Ala Phe Leu Ala Leu Ala Ile Ile Leu Leu Gly Arg
 260 265 270
 Gly Ile Lys Phe Lys Glu Thr Asp Ser Leu Met Asp Asp Ser Val Lys
 275 280 285
 Met Met Ala Phe Ile Ala Phe Val Met Leu Val Ala Ser Gly Phe Gly
 290 295 300
 Glu Val Leu Gln Lys Val His Ala Ile Glu Gly Leu Val Asn Ala Ile
 305 310 315 320
 Thr Ser Val Val Gln Gly Lys Leu Leu Gly Ala Phe Leu Met Leu Val
 325 330 335
 Val Gly Leu Phe Ile Thr Met Gly Ile Gly Thr Ser Phe Gly Thr Ile
 340 345 350
 Pro Ile Ile Ala Val Phe Tyr Val Pro Leu Cys Ala Lys Leu Gly Phe
 355 360 365
 Ser Val Glu Ser Thr Ile Leu Leu Ile Ala
 370 375

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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (61)...(636)

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 gtg ggg tta gta acc acg aca ttg gct tta ggg att tct tgc atc att 108
 Val Gly Leu Val Thr Thr Leu Ala Leu Gly Ile Ser Cys Ile Ile
 1 5 10 15
 tta ttc gtg gcg ttt ttt agc atc att tgg cgg att ttg gct ttg att 156
 Leu Phe Val Ala Phe Phe Ser Ile Ile Trp Arg Ile Leu Ala Leu Ile
 20 25 30
 tct ggg ttc cct tct tgc tgt ttg tat tcg tcc tta act tct tgt tta 204
 Ser Gly Phe Pro Ser Cys Cys Leu Tyr Ser Ser Leu Thr Ser Cys Leu
 35 40 45
 gtc att ttt aaa gag ttg gtg tat tgg cgg cgt ttg atc gct aaa tct 252
 Val Ile Phe Lys Glu Leu Val Tyr Trp Arg Arg Leu Ile Ala Lys Ser
 50 55 60
 ata aaa gcc aag aca aaa aat aaa aat aaa agc gaa gaa atg agc cat 300
 Ile Lys Ala Lys Thr Lys Asn Lys Asn Lys Ser Glu Glu Met Ser His
 65 70 75 80
 aac gcc tta ttt tta aac cac aac aac tgg cct tgt aaa ttc aaa aga 348
 Asn Ala Leu Phe Leu Asn His Asn Asn Trp Pro Cys Lys Phe Lys Arg
 85 90 95

Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser
 165 170 175
 180 185 190

<210> 47
 <211> 851
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (49)...(783)

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 Met Asn Phe
 1
 tat caa aaa ata tac act cat aaa gtc gtt ttt tct tca ttg ttt ttt 105
 Tyr Gln Lys Ile Tyr Thr His Lys Val Val Phe Ser Ser Leu Phe Phe
 5 10 15
 ttg ttg ttt ttg ttc aat gtg gaa act ttg ttg ctt tcg cat ttc agc 153
 Leu Leu Phe Leu Phe Asn Val Glu Thr Leu Leu Leu Ser His Phe Ser
 20 25 30 35
 gat gat ttt tcg caa ttg ttt ttt ttg ttt gaa aac cat gtt tat gat 201
 Asp Asp Phe Ser Gln Leu Phe Phe Leu Phe Glu Asn His Val Tyr Asp
 40 45 50
 ttc att gtc aaa tta gat tat ttg ggg cta ata ggc gtt tct tta att 249
 Phe Ile Val Lys Leu Asp Tyr Leu Gly Leu Ile Gly Val Ser Leu Ile
 55 60 65
 tat ctg ctt gtg ctt att cta aag cct ttc acc ctc acg cgc caa aaa 297
 Tyr Leu Leu Val Leu Ile Leu Lys Pro Phe Thr Leu Thr Arg Gln Lys
 70 75 80
 tgc gct tgc gta ggg ata tta tgc ctt tct ttc tac gct tgg aat ttt 345
 Cys Ala Cys Val Gly Ile Leu Cys Leu Ser Phe Tyr Ala Trp Asn Phe
 85 90 95
 cct gtt aaa gat tct tta atg gtg ctt tat ctt ttc tat ttt gcg ctg 393
 Pro Val Lys Asp Ser Leu Met Val Leu Tyr Leu Phe Tyr Phe Ala Leu
 100 105 110 115
 tta gcg act tta ttg tgg cgt ttt tta ggg gct agc atg aag caa tct 441
 Leu Ala Thr Leu Leu Trp Arg Phe Leu Gly Ala Ser Met Lys Gln Ser
 120 125 130
 ttc ttg ccc tct atg aat att tgc atc gtg tgg gtt ttt gct tct tct 489
 Phe Leu Pro Ser Met Asn Ile Cys Ile Val Trp Val Phe Ala Ser Ser
 135 140 145
 tta cag agt ttt agg ttt tta agc gtg tct gat tgc gtg gat ttt tcc 537
 Leu Gln Ser Phe Arg Phe Leu Ser Val Ser Asp Cys Val Asp Phe Ser
 150 155 160
 ctt ttt aca ctc gcg ctt att tta ttg ata ctg gtt tta atc tat tgc 585

Leu	Phe	Thr	Leu	Ala	Leu	Ile	Leu	Ile	Leu	Val	Leu	Ile	Tyr	Cys		
165						170				175						
aaa	cgc	ctt	ttt	ggg	ttg	tat	gaa	tac	gct	aac	acg	ctc	att	ttg	atc	633
Lys	Arg	Leu	Phe	Gly	Leu	Tyr	Glu	Tyr	Ala	Asn	Thr	Leu	Ile	Leu	Ile	
180				185						190					195	
gtg	ggg	ctt	agc	gtg	gtg	gtg	cta	tgc	tct	agc	atg	ttc	att	caa	act	681
Val	Gly	Leu	Ser	Val	Val	Val	Leu	Cys	Ser	Ser	Met	Phe	Ile	Gln	Thr	
				200					205					210		
aaa	gaa	tac	tat	ggc	atg	cga	ttg	ggt	ttt	tat	ttt	tta	ggc	ctg	tta	729
Lys	Glu	Tyr	Tyr	Gly	Met	Arg	Leu	Gly	Phe	Tyr	Phe	Leu	Gly	Leu	Leu	
			215					220					225			
ggg	tgg	ctt	tta	gaa	tat	gtg	cat	aac	act	tta	agg	cgt	ttg	gaa	cat	777
Gly	Trp		Leu	Glu	Tyr	Val	His	Asn	Thr	Leu	Arg	Arg	Leu	Glu	His	
		230					235					240				
caa	att	taa	agctcaa	ataggaatag	ctaaagcctt	ttgattgagt	gttttttttag									833
Gln	Ile															
		245														
ggc	tta	aaaag	cgggttta													851
<210>	48															
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<213>	Helicobacter pylori															
<400>	48															
Met	Asn	Phe	Tyr	Gln	Lys	Ile	Tyr	Thr	His	Lys	Val	Val	Phe	Ser	Ser	
1				5					10					15		
Leu	Phe	Phe	Leu	Phe	Leu	Phe	Asn	Val	Glu	Thr	Leu	Leu	Leu	Leu	Ser	
			20					25					30			
His	Phe	Ser	Asp	Asp	Phe	Ser	Gln	Leu	Phe	Phe	Leu	Phe	Glu	Asn	His	
		35					40					45				
Val	Tyr	Asp	Phe	Ile	Val	Lys	Leu	Asp	Tyr	Leu	Gly	Leu	Ile	Gly	Val	
	50					55					60					
Ser	Leu	Ile	Tyr	Leu	Leu	Val	Leu	Ile	Leu	Lys	Pro	Phe	Thr	Leu	Thr	
65					70					75					80	
Arg	Gln	Lys	Cys	Ala	Cys	Val	Gly	Ile	Leu	Cys	Leu	Ser	Phe	Tyr	Ala	
			85					90						95		
Trp	Asn	Phe	Pro	Val	Lys	Asp	Ser	Leu	Met	Val	Leu	Tyr	Leu	Phe	Tyr	
			100					105					110			
Phe	Ala	Leu	Leu	Ala	Thr	Leu	Leu	Trp	Arg	Phe	Leu	Gly	Ala	Ser	Met	
		115					120					125				
Lys	Gln	Ser	Phe	Leu	Pro	Ser	Met	Asn	Ile	Cys	Ile	Val	Trp	Val	Phe	
	130					135					140					

Gly Leu Leu Gly Trp Leu Leu Glu Tyr Val His Asn Thr Leu Arg Arg
 225 230 235 240
 Leu Glu His Gln Ile
 245

<210> 49
 <211> 827
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (95)...(745)

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 ttaagtgcgt tttggtaaaa ttgattatatt gaac atg ctc cct ttt gat gtg ttt 115
 Met Leu Pro Phe Asp Val Phe
 1 5

atc aaa tcc tac ccc acc cct tgt tat ttc aaa caa ttc tta cgg ctt 163
 Ile Lys Ser Tyr Pro Thr Pro Cys Tyr Phe Lys Gln Phe Leu Arg Leu
 10 15 20

aaa aaa acc tac ccc tcc aaa ctc aat gag agt ttt tta ttc agg cgt 211
 Lys Lys Thr Tyr Pro Ser Lys Leu Asn Glu Ser Phe Leu Phe Arg Arg
 25 30 35

att gat gcg ggg ttt att tct tct atc gcc ggc tat cca ttc gct ctt 259
 Ile Asp Ala Gly Phe Ile Ser Ser Ile Ala Gly Tyr Pro Phe Ala Leu
 40 45 50 55

cat tcc cat tct cta ggc att gtc gct tat aag gaa gtt tta agc gtg 307
 His Ser His Ser Leu Gly Ile Val Ala Tyr Lys Glu Val Leu Ser Val
 60 65 70

ctg gtt gtg gat aca aaa aac gct ttt gat aaa gaa agc gct tct tca 355
 Leu Val Val Asp Thr Lys Asn Ala Phe Asp Lys Glu Ser Ala Ser Ser
 75 80 85

aac gcc ctc tct caa gcg cta ggg tta aag ggc gaa gtg tta atc ggc 403
 Asn Ala Leu Ser Gln Ala Leu Gly Leu Lys Gly Glu Val Leu Ile Gly
 90 95 100

aat aaa gca ctg cag ttt tat tat tcc aac cct aaa aaa gat ttt ata 451
 Asn Lys Ala Leu Gln Phe Tyr Tyr Ser Asn Pro Lys Lys Asp Phe Ile
 105 110 115

gat tta gcc gct ctt tgg tat gaa aaa aaa cgc ttg ccg ttt gtt ttt 499
 Asp Leu Ala Ala Leu Trp Tyr Glu Lys Lys Arg Leu Pro Phe Val Phe
 120 125 130 135

ggg cgt ttg tgt tat tac caa aac aag gat ttt tac aag cgc ttg tct 547
 Gly Arg Leu Cys Tyr Tyr Gln Asn Lys Asp Phe Tyr Lys Arg Leu Ser
 140 145 150

tta gct ttc aaa cat caa aaa aca aaa atc cct tac tac atc ctt aaa 595
 Leu Ala Phe Lys His Gln Lys Thr Lys Ile Pro Tyr Tyr Ile Leu Lys
 155 160 165

[illegible]

-64-

<210> 52
 <211> 196
 <212> PRT
 <213> Helicobacter pylori

<400> 52
 Met Met Gly Tyr Ile Pro Tyr Val Ile Glu Asn Thr Asp Arg Gly Glu
 1 5 10 15
 Arg Ser Tyr Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Val Leu
 20 25 30
 Leu Ser Gly Glu Ile Asn Asp Ser Val Ala Ser Ser Ile Val Ala Gln
 35 40 45
 Leu Leu Phe Leu Glu Ala Glu Asp Pro Glu Lys Asp Ile Gly Leu Tyr
 50 55 60
 Ile Asn Ser Pro Gly Gly Val Ile Thr Ser Gly Leu Ser Ile Tyr Asp
 65 70 75 80
 Thr Met Asn Phe Ile Arg Pro Asp Val Ser Thr Ile Cys Ile Gly Gln
 85 90 95
 Ala Ala Ser Met Gly Ala Phe Leu Leu Ser Cys Gly Ala Lys Gly Lys
 100 105 110
 Arg Phe Ser Leu Pro His Ser Arg Ile Met Ile His Gln Pro Leu Gly
 115 120 125
 Gly Ala Gln Gly Gln Ala Ser Asp Ile Glu Ile Ile Ser Asn Glu Ile
 130 135 140
 Leu Arg Leu Lys Gly Leu Met Asn Ser Ile Leu Ala Gln Asn Ser Gly
 145 150 155 160
 Gln Ser Leu Glu Gln Ile Ala Lys Asp Thr Asp Arg Asp Phe Tyr Met
 165 170 175
 Ser Ala Lys Glu Ala Lys Glu Tyr Gly Leu Ile Asp Lys Val Leu Gln
 180 185 190
 Lys Asn Val Lys
 195

<210> 53
 <211> 904
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(852)

<400> 53
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 Arg Ile Lys Lys Glu Arg Leu Asn Lys Leu Leu Lys Arg Gly Phe Leu
 1 5 10 15
 gcg ttc ttt ttg agc gtg tat tta agg gct gat gat ttg gtt act tac 96
 Ala Phe Phe Leu Ser Val Tyr Leu Arg Ala Asp Asp Leu Val Thr Tyr
 20 25 30
 acc atc atc aaa gaa aaa gat cta gga tac cag cgg ttt tta gcc aag 144
 Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys
 35 40 45
 aag tgt tta agg ggt aaa acc cac cct ccg tgt ttt act aag cct aaa 192
 Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys
 50 55 60

aag cct aaa aga aaa ctt ttt aat ata gac aaa agc tcc cac tat tat	240
Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr	
65 70 75 80	
ggc aca agc gtg gtg caa atg tca tgg cta cag agt agg gaa aaa ttt	288
Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe	
85 90 95	
gaa aac cat tca aaa tac cga gac att cct ttt gct gaa gtc agt ttg	336
Glu Asn His Ser Lys Tyr Arg Asp Ile Pro Phe Ala Glu Val Ser Leu	
100 105 110	
att tat ggc tat aaa caa ttt ttt cct aaa aaa gag cgc tac ggc ttc	384
Ile Tyr Gly Tyr Lys Gln Phe Phe Pro Lys Lys Glu Arg Tyr Gly Phe	
115 120 125	
cgt ttt tat gtc tct ttg gat tac gct tat ggg ttt ttt ctt aaa aat	432
Arg Phe Tyr Val Ser Leu Asp Tyr Ala Tyr Gly Phe Phe Leu Lys Asn	
130 135 140	
aag ggc gtg ttg ggc gat agt ttg agg gag agt tcg caa atc cct aaa	480
Lys Gly Val Leu Gly Asp Ser Leu Arg Glu Ser Ser Gln Ile Pro Lys	
145 150 155 160	
agc tat aga gaa aaa ttg caa aga aaa gag act ttt att aac gct att	528
Ser Tyr Arg Glu Lys Leu Gln Arg Lys Glu Thr Phe Ile Asn Ala Ile	
165 170 175	
ttt tat ggc gcg gga gct gac ttt tta tac aaa cgc gct ttt gga acg	576
Phe Tyr Gly Ala Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly Thr	
180 185 190	
ctg att tta ggg atg aat ttc gtg gga gaa acc tgg ttt tat gaa aca	624
Leu Ile Leu Gly Met Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu Thr	
195 200 205	
aag att ttt aaa aag tgg gct aaa gat cct ttg agc gtt tat cac cct	672
Lys Ile Phe Lys Lys Trp Ala Lys Asp Pro Leu Ser Val Tyr His Pro	
210 215 220	
tac atg ttt caa gtg atg ttg aat gtg ggg tat cgt tac cgc ttt tca	720
Tyr Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe Ser	
225 230 235 240	
agg tat aag aat tgg gcg ata gaa ttg ggt gcg cgc atc cct ttt tta	768
Arg Tyr Lys Asn Trp Ala Ile Glu Leu Gly Ala Arg Ile Pro Phe Leu	
245 250 255	
acc aat gat tat ttt aaa acc cct tta tac acc ctt cat ttc aag cgc	816
Thr Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys Arg	
260 265 270	
aat att tct gtc tat ctc act tca act tat gac ttt tagttttttta	862
Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe	
275 280	
aattttttgaa aactagaatt aaaaccgctt tttataaact gg	904

<210> 54

<211> 284
 <212> PRT
 <213> Helicobacter pylori

<400> 54

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Ala	Phe	Phe	Leu	Ser	Val	Tyr	Leu	Arg	Ala	Asp	Asp	Leu	Val	Thr	Tyr
			20					25					30		
Thr	Ile	Ile	Lys	Glu	Lys	Asp	Leu	Gly	Tyr	Gln	Arg	Phe	Leu	Ala	Lys
		35					40					45			
Lys	Cys	Leu	Arg	Gly	Lys	Thr	His	Pro	Pro	Cys	Phe	Thr	Lys	Pro	Lys
	50					55					60				
Lys	Pro	Lys	Arg	Lys	Leu	Phe	Asn	Ile	Asp	Lys	Ser	Ser	His	Tyr	Tyr
65					70				75						80
Gly	Thr	Ser	Val	Val	Gln	Met	Ser	Trp	Leu	Gln	Ser	Arg	Glu	Lys	Phe
				85					90					95	
Glu	Asn	His	Ser	Lys	Tyr	Arg	Asp	Ile	Pro	Phe	Ala	Glu	Val	Ser	Leu
			100					105					110		
Ile	Tyr	Gly	Tyr	Lys	Gln	Phe	Phe	Pro	Lys	Lys	Glu	Arg	Tyr	Gly	Phe
		115					120						125		
Arg	Phe	Tyr	Val	Ser	Leu	Asp	Tyr	Ala	Tyr	Gly	Phe	Phe	Leu	Lys	Asn
		130				135						140			
Lys	Gly	Val	Leu	Gly	Asp	Ser	Leu	Arg	Glu	Ser	Ser	Gln	Ile	Pro	Lys
145					150					155					160
Ser	Tyr	Arg	Glu	Lys	Leu	Gln	Arg	Lys	Glu	Thr	Phe	Ile	Asn	Ala	Ile
				165					170					175	
Phe	Tyr	Gly	Ala	Gly	Ala	Asp	Phe	Leu	Tyr	Lys	Arg	Ala	Phe	Gly	Thr
			180					185					190		
Leu	Ile	Leu	Gly	Met	Asn	Phe	Val	Gly	Glu	Thr	Trp	Phe	Tyr	Glu	Thr
		195					200					205			
Lys	Ile	Phe	Lys	Lys	Trp	Ala	Lys	Asp	Pro	Leu	Ser	Val	Tyr	His	Pro
	210					215					220				
Tyr	Met	Phe	Gln	Val	Met	Leu	Asn	Val	Gly	Tyr	Arg	Tyr	Arg	Phe	Ser
225					230					235					240
Arg	Tyr	Lys	Asn	Trp	Ala	Ile	Glu	Leu	Gly	Ala	Arg	Ile	Pro	Phe	Leu
				245					250					255	
Thr	Asn	Asp	Tyr	Phe	Lys	Thr	Pro	Leu	Tyr	Thr	Leu	His	Phe	Lys	Arg
			260					265					270		
Asn	Ile	Ser	Val	Tyr	Leu	Thr	Ser	Thr	Tyr	Asp	Phe				
		275					280								

<210> 55
 <211> 1172
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (75)...(1106)

<400> 55

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actagggagt	taga	atg	atc	tta	aaa	cga	gtt	act	gaa	gct	tta	gaa	gcg		110
		Met	Ile	Leu	Lys	Arg	Val	Thr	Glu	Ala	Leu	Glu	Ala		
		1				5						10			
tat	aaa	aat	ggc	gaa	atg	ctc	att	gtt	atg	gac	gat	gaa	gac	aga	gaa
Tyr	Lys	Asn	Gly	Glu	Met	Leu	Ile	Val	Met	Asp	Asp	Glu	Asp	Arg	Glu

15	20	25	
aat gag ggg gat ttg gtt tta gct ggg att ttt tct acc cct gag aaa			206
Asn Glu Gly Asp Leu Val Leu Ala Gly Ile Phe Ser Thr Pro Glu Lys			
30	35	40	
atc aat ttc atg gcc acg cat gct agg ggg ttg att tgc gtg tct ttg			254
Ile Asn Phe Met Ala Thr His Ala Arg Gly Leu Ile Cys Val Ser Leu			
45	50	55	60
acc aaa gat tta gcg aaa aaa ttt gaa tta ccc cct atg gtt agc gtg			302
Thr Lys Asp Leu Ala Lys Lys Phe Glu Leu Pro Pro Met Val Ser Val			
65	70	75	
aat gat tct aac cat gag acc gct ttc acg gtt tcc att gac gct aaa			350
Asn Asp Ser Asn His Glu Thr Ala Phe Thr Val Ser Ile Asp Ala Lys			
80	85	90	
gaa gcc aga acc ggg att tct gct ttt gaa agg cat tta acg att gaa			398
Glu Ala Arg Thr Gly Ile Ser Ala Phe Glu Arg His Leu Thr Ile Glu			
95	100	105	
tta ttg tgt aaa gac acc acc aaa ccg agc gat ttt gtg cgc ccg ggg			446
Leu Leu Cys Lys Asp Thr Thr Lys Pro Ser Asp Phe Val Arg Pro Gly			
110	115	120	
cat att ttc cct ttg atc gcc aaa gac ggg ggc gtg tta gcg cgc acg			494
His Ile Phe Pro Leu Ile Ala Lys Asp Gly Gly Val Leu Ala Arg Thr			
125	130	135	140
ggc cat act gaa gcg agc gtg gat ttg tgc aaa tta gct gga tta aag			542
Gly His Thr Glu Ala Ser Val Asp Leu Cys Lys Leu Ala Gly Leu Lys			
145	150	155	
ccc gtg agc gtg att tgt gaa atc atg aaa gaa gat ggc tct atg gcg			590
Pro Val Ser Val Ile Cys Glu Ile Met Lys Glu Asp Gly Ser Met Ala			
160	165	170	
aga agg ggg gat aaa ttt ttg agc gat ttc gcc ctc aaa cat aac ctt			638
Arg Arg Gly Asp Lys Phe Leu Ser Asp Phe Ala Leu Lys His Asn Leu			
175	180	185	
aaa act ctc tat gtc tct gat ttg att agc tat cgt ttg gaa aat gaa			686
Lys Thr Leu Tyr Val Ser Asp Leu Ile Ser Tyr Arg Leu Glu Asn Glu			
190	195	200	
agt ttg ctg aaa atg ttt tgt caa gaa gaa agg gaa ttt tta aaa cac			734
Ser Leu Leu Lys Met Phe Cys Gln Glu Glu Arg Glu Phe Leu Lys His			
205	210	215	220
caa acg caa tgc tac act ttt tta gat cac cag caa aaa aac cat tac			782
Gln Thr Gln Cys Tyr Thr Phe Leu Asp His Gln Gln Lys Asn His Tyr			
225	230	235	
gct ttt aag ttt aaa ggc gca aaa acc cat gat tta gcc cct tta gtg			830
Ala Phe Lys Phe Lys Gly Ala Lys Thr His Asp Leu Ala Pro Leu Val			
240	245	250	
cgt ttc cac cct atc aaa gag gat ttt gat ttt tta acg act gat gcg			878

Tyr	Thr	Phe	Leu	Asp	His	Gln	Gln	Lys	Asn	His	Tyr	Ala	Phe	Lys	Phe
225					230					235					240
Lys	Gly	Ala	Lys	Thr	His	Asp	Leu	Ala	Pro	Leu	Val	Arg	Phe	His	Pro
				245					250					255	
Ile	Lys	Glu	Asp	Phe	Asp	Phe	Leu	Thr	Thr	Asp	Ala	Phe	Glu	Val	Phe
			260					265					270		
Phe	Lys	Ala	Leu	Glu	Tyr	Leu	Lys	His	Glu	Gly	Gly	Tyr	Leu	Ile	Phe
		275						280				285			
Met	Asn	Thr	His	Ser	Lys	Glu	Asn	Asn	Val	Val	Lys	Asp	Phe	Gly	Ile
	290					295					300				
Gly	Ala	Leu	Val	Leu	Lys	Asn	Leu	Gly	Ile	Lys	Asp	Phe	Arg	Leu	Leu
305					310					315					320
Ser	Ser	Cys	Glu	Asp	Arg	Gln	Tyr	Lys	Ala	Leu	Ser	Gly	Phe	Gly	Leu
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Lys	Leu	Val	Glu	Thr	Ile	Ser	Leu								
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 <212> DNA
 <213> Helicobacter pylori

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	Lys Leu
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cat ttt aaa gcg ttt cac gca ctt ttc tat cct agc aat aga gac aat	104
His Phe Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg Asp Asn	
5	10 15
atc tat gcc aat cat tta aaa tta ttg gat aat gaa atc agt gaa aaa	152
Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser Glu Lys	
20	25 30
gac att ttt aat aaa gcc atc aat caa aaa cga att caa atg gct ctt	200
Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met Ala Leu	
35	40 45 50
aat ctc atc ttt aag ctt gtt ttt gcc ttt gtt agt aac cac ttc ttc	248
Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His Phe Phe	
	55 60 65
cac gct ttt aga cga cag aat ctc tat aat cgt gtc ttt aat cgc tgt	296
His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn Arg Cys	
	70 75 80
gtc ttt aac ctt gac ttc att caa aag ctt ttc att act caa ttc	341
Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln Phe	
	85 90 95
taacgaaata gaagccttaa ggtagcgtct gccattttga gagaccagat tca	394

<210> 58
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[illegible]

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1				5					10				15
Leu	Val	Ala	Ile	Thr	Ile	Gln	Ala	Cys	Gly	Tyr	Lys	Ala	Pro
			20					25				30	
Asn	Glu	Lys	Pro	Ala	Lys	Lys	Thr	Ser	Asn	Ser	Ser	Asn	Ser
		35					40					45	
Gln	Thr	Pro	Thr	Asn	Ser	Thr	Thr	Pro	Glu	Phe	Leu	Asn	Gln
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<220>
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	Met Arg
	1

ttt ttg aac aac aaa cat aga gaa aag ggc tta aag gct gaa gaa gaa	104
Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu Glu Glu	
	5 10 15

gct tgc gga ttt tta aaa tcg tta ggt ttt gaa atg gtg gag agg aac	152
Ala Cys Gly Phe Leu Lys Ser Leu Gly Phe Glu Met Val Glu Arg Asn	
	20 25 30

ttt ttt tca caa ttt ggc gaa att gat att atc gct ttg aaa aaa ggg	200
Phe Phe Ser Gln Phe Gly Glu Ile Asp Ile Ile Ala Leu Lys Lys Gly	
	35 40 45 50

gtt ttg cat ttc att gaa gtc aaa agc ggg gaa aat ttt gat ccc att	248
Val Leu His Phe Ile Glu Val Lys Ser Gly Glu Asn Phe Asp Pro Ile	
	55 60 65

tat gcg atc acg ccg agc aaa tta aaa aag atg att aaa acg atc cgc	296
Tyr Ala Ile Thr Pro Ser Lys Leu Lys Lys Met Ile Lys Thr Ile Arg	
	70 75 80

tgt tat ttg tcc caa aaa gat ccc aat agc gat ttt tgc ata gac gct	344
Cys Tyr Leu Ser Gln Lys Asp Pro Asn Ser Asp Phe Cys Ile Asp Ala	
	85 90 95

ctt att gtg aaa aat ggt aaa ttt gag ctt tta gaa aat atc act ttt	392
Leu Ile Val Lys Asn Gly Lys Phe Glu Leu Leu Glu Asn Ile Thr Phe	
	100 105 110

tagattttta cagaaagtaa atgcgatttc attaacattc ttaagctaata ata	445
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<210> 62
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 <212> PRT
 <213> Helicobacter pylori

<400> 62
Met Arg Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu

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<222> (86) ... (763)
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-73-

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gca ggt cct gtg aaa tgg ctc gcc cct ttc atg ttc cct att gag atc Ala Gly Pro Val Lys Trp Leu Ala Pro Phe Met Phe Pro Ile Glu Ile 140 145 150	544
atc tcg cat ttt tct agg atc gtg tct tta tcg ttt cgt ttg ttt ggg Ile Ser His Phe Ser Arg Ile Val Ser Leu Ser Phe Arg Leu Phe Gly 155 160 165	592
aat atc aag ggc gat gac atg ttc ttg ctc atc atg ctt tta tta gtg Asn Ile Lys Gly Asp Asp Met Phe Leu Leu Ile Met Leu Leu Leu Val 170 175 180 185	640
cct tgg gcg gtt cct gta gcg cct ttt atg gtg ttg ttt ttc atg ggg Pro Trp Ala Val Pro Val Ala Pro Phe Met Val Leu Phe Phe Met Gly 190 195 200	688
att tta caa gct ttt gtt ttt atg atc ctc act tat gtg tat ttg gca Ile Leu Gln Ala Phe Val Phe Met Ile Leu Thr Tyr Val Tyr Leu Ala 205 210 215	736
ggg gct gtt tta acc gat gaa ggg cat taagcaataa cattcttggt Gly Ala Val Leu Thr Asp Glu Gly His 220 225	783
tggtcttaaat attgtttttt aaaactttgt tttatggtaa agcttttta	831
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Asp Phe Ile Thr Gly Phe Phe Val Val Leu Thr Ala Val Leu Met Phe 20 25 30	
Leu Ile Ser Leu Gly Ala Ser Arg Lys Met Gln Met Val Pro Met Gly 35 40 45	
Leu Gln Asn Val Tyr Glu Ser Ile Ile Ser Ala Ile Leu Ser Val Ala 50 55 60	
Lys Asp Ile Ile Gly Glu Glu Leu Ala Arg Lys Tyr Phe Pro Leu Ala 65 70 75 80	
Gly Thr Ile Ala Leu Tyr Val Phe Phe Ser Asn Met Ile Gly Ile Ile 85 90 95	
Pro Gly Phe Glu Ser Pro Thr Ala Ser Trp Ser Phe Thr Leu Val Leu 100 105 110	
Ala Leu Ile Val Phe Phe Tyr Tyr His Phe Glu Gly Ile Arg Val Gln 115 120 125	
Gly Phe Phe Lys Tyr Phe Ala His Phe Ala Gly Pro Val Lys Trp Leu 130 135 140	
Ala Pro Phe Met Phe Pro Ile Glu Ile Ile Ser His Phe Ser Arg Ile 145 150 155 160	
Val Ser Leu Ser Phe Arg Leu Phe Gly Asn Ile Lys Gly Asp Asp Met 165 170 175	
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-75-

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att	att	tta	gac	acc	aaa	aac	gcc	ctt	tta	gca	tgc	gac	act	aaa	ggc		584
Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr	Lys	Gly		
		165					170					175					
gat	ggg	gcg	atg	gct	gag	cct	tta	gaa	atc	ctt	ttt	aaa	gcc	gct	caa		632
Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala	Ala	Gln		
	180					185					190						
acg	ctc	cta	aaa	gac	gct	tat	ttt	gaa	aac	aga	gaa	gtc	ata	gtc	atg		680
Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile	Val	Met		
	195				200					205					210		
ggc	ggc	gcg	agt	ata	gaa	aag	att	gac	agc	gtt	cga	acg	att	agc	aat		728
Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile	Ser	Asn		
				215				220						225			
act	ttc	tagcgggatt	caagcgagcg	ctttagcttt	ggcgttatat	tttaagggag											784
Thr	Phe																

cca

787

<210> 66
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 <212> PRT
 <213> Helicobacter pylori

<400> 66

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		20						25					30				
Leu	Glu	Leu	Val	Arg	Leu	Leu	Phe	Lys	Ser	Gly	Ala	Ser	Ile	Gln	Val		
	35					40						45					
Val	Met	Ser	Lys	Gly	Ala	Lys	Phe	Ile	Lys	Pro	Leu	Ser	Phe	Glu			
	50					55				60							
Ala	Leu	Ser	His	His	Lys	Val	Leu	His	Asp	Arg	Asn	Glu	Lys	Trp	Tyr		
65				70					75					80			
Tyr	Asn	His	Gln	Asn	Ala	Leu	His	His	Asn	His	Ile	Ala	Cys	Ala	Ala		
			85					90					95				
Asn	Ala	Asp	Leu	Leu	Ile	Phe	Ala	Pro	Leu	Ser	Thr	Asn	Ser	Leu	Ser		
		100					105					110					
Lys	Ile	Ala	His	Ala	Leu	Ala	Asp	Asn	Ile	Val	Ser	Ala	Thr	Phe	Leu		
	115					120						125					
Ala	Cys	Ala	Ser	Pro	Lys	Ile	Leu	Ala	Pro	Ser	Met	Asn	Thr	Asn	Met		
	130				135						140						
Leu	Asn	Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser		
145				150						155				160			
Asn	His	Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr		
			165				170						175				
Lys	Gly	Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala		
	180						185					190					
Ala	Gln	Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile		
	195					200					205						
Val	Met	Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile		
	210					215					220						

Ser Asn Thr Phe
225

<210> 67
<211> 1078
<212> DNA
<213> Helicobacter pylori

<220>
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<222> (71)...(1009)

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cgagcaaaaa atg aaa ccg caa gac att gaa atc gtt caa agc gtt tta 109
Met Lys Pro Gln Asp Ile Glu Ile Val Gln Ser Val Leu
1 5 10

gag att aca gga ccg att aag cct act gaa gtg tat gat aaa gcc aaa 157
Glu Ile Thr Gly Pro Ile Lys Pro Thr Glu Val Tyr Asp Lys Ala Lys
15 20 25

gag ctt ttt gaa aaa ggt gag att aca aac atg ttt gat tgt ggg ggc 205
Glu Leu Phe Glu Lys Gly Glu Ile Thr Asn Met Phe Asp Cys Gly Gly
30 35 40 45

aaa acc ccg cac cag agc gtt agt tct tat att tat aca gcc tta aac 253
Lys Thr Pro His Gln Ser Val Ser Ser Tyr Ile Tyr Thr Ala Leu Asn
50 55 60

aag ggc gaa gaa ctg cct ttt aaa aaa gtg caa gaa aac cca acc tta 301
Lys Gly Glu Glu Leu Pro Phe Lys Lys Val Gln Glu Asn Pro Thr Leu
65 70 75

atc gct tta aaa gac gcg gct aaa gag cta ggt tta gac gct caa aaa 349
Ile Ala Leu Lys Asp Ala Ala Lys Glu Leu Gly Leu Asp Ala Gln Lys
80 85 90

ata agc gct cca agc tct aaa atc gcg cat gaa agg gat ttg cac ccc 397
Ile Ser Ala Pro Ser Ser Lys Ile Ala His Glu Arg Asp Leu His Pro
95 100 105

ttt tta acc tac atg gct att aat aac gaa aat ttg aaa tgc tac acg 445
Phe Leu Thr Tyr Met Ala Ile Asn Asn Glu Asn Leu Lys Cys Tyr Thr
110 115 120 125

aaa acc att ttt cat gaa gag agt tca aaa tca ata aaa ggc atg gac 493
Lys Thr Ile Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp
130 135 140

agg tgg ctt tat ccg gac atg gtg ggg gtt agg ttt ttg cac gct gaa 541
Arg Trp Leu Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu
145 150 155

tta tct aat gaa aat tta atc gct ttt tct aag aaa ttt gac act tta 589
Leu Ser Asn Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu
160 165 170

ccc att aaa ctg gtg agc ttt gaa ttg aaa aaa gaa atc agc gtg cat 637

Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr	Tyr	Thr	Leu	Lys	Asp	Phe	Glu		
			75					80					85				
caa	ctc	acc	caa	tac	ctc	caa	gaa	agc	ttg	ttc	aaa	gaa	tta	ggg	ttt	461	
Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser	Leu	Phe	Lys	Glu	Leu	Gly	Phe		
		90					95					100					
aat	ctg	gat	ggc	atc	tat	ttt	tgc	agg	cac	gcc	cca	gaa	gaa	aat	tgc	509	
Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg	His	Ala	Pro	Glu	Glu	Asn	Cys		
	105					110					115						
gct	tgc	agg	aag	cca	aag	cct	tct	ttg	att	ttg	caa	gct	gct	aaa	gag	557	
Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu	Ile	Leu	Gln	Ala	Ala	Lys	Glu		
120					125					130					135		
cat	caa	att	tgc	ttg	gag	caa	tct	ttt	atg	ata	ggc	gat	aaa	gag	agc	605	
His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe	Met	Ile	Gly	Asp	Lys	Glu	Ser		
			140					145						150			
gac	atg	tta	gcc	ggc	ttg	aac	gct	aaa	gtt	aaa	aat	aac	ctt	ttg	ctc	653	
Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys	Val	Lys	Asn	Asn	Leu	Leu	Leu		
			155					160					165				
att	caa	aac	cct	tta	aaa	act	cct	cat	tct	tgg	ata	caa	tgt	aaa	gat	701	
Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His	Ser	Trp	Ile	Gln	Cys	Lys	Asp		
		170					175					180					
ttt	aaa	gag	atg	ata	gat	cta	atc	aaa	taaggacaag	aatgcggttat						748	
Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys									
	185					190											
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<213>	Helicobacter pylori																
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Met	Pro	Cys	Ile	Ile	Lys	Thr	Thr	Pro	Leu	Ser	Met	Ile	Ile	Lys	Glu		
1				5					10					15			
Cys	Ile	Arg	Met	Asn	Thr	Asn	Lys	Ala	Leu	Phe	Leu	Asp	Arg	Asp	Gly		
			20					25					30				
Ile	Ile	Asn	Ile	Asp	Lys	Gly	Tyr	Val	Ser	Gln	Lys	Glu	Asp	Phe	Glu		
		35				40						45					
Phe	Gln	Lys	Gly	Ile	Phe	Glu	Leu	Leu	Lys	His	Ala	Lys	Ser	Leu	Gly		
	50					55				60							
Tyr	Lys	Leu	Leu	Leu	Ile	Thr	Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr		
65					70					75					80		
Tyr	Thr	Leu	Lys	Asp	Phe	Glu	Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser		
			85						90					95			
Leu	Phe	Lys	Glu	Leu	Gly	Phe	Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg		
		100						105					110				
His	Ala	Pro	Glu	Glu	Asn	Cys	Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu		
		115					120					125					
Ile	Leu	Gln	Ala	Ala	Lys	Glu	His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe		
	130					135					140						
Met	Ile	Gly	Asp	Lys	Glu	Ser	Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys		

145		150		155		160									
Val	Lys	Asn	Asn	Leu	Leu	Leu	Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His
		165				170								175	
Ser	Trp	Ile	Gln	Cys	Lys	Asp	Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys
		180				185							190		

<210> 73
 <211> 831
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (88)...(756)

<400> 73

aacaaagagc	gagagagcat	caagaaagag	atgaaaaaga	gcttgaagaa	agaagaaaag	60
ctttagaaat	gaataagaag	taggcct	atg cca gct agg	caa tct ttt aca	gat	114
			Met Pro Ala Arg	Gln Ser Phe Thr	Asp	
			1		5	

ttg	aaa	aac	ctg	gtt	ttg	tgc	gat	ata	ggc	aac	acg	cgt	atc	cat	ttt	162
Leu	Lys	Asn	Leu	Val	Leu	Cys	Asp	Ile	Gly	Asn	Thr	Arg	Ile	His	Phe	
10					15					20					25	

gca	caa	aac	tat	cag	ctc	ttt	tca	agc	gct	aaa	gaa	gat	tta	aag	cgt	210
Ala	Gln	Asn	Tyr	Gln	Leu	Phe	Ser	Ser	Ala	Lys	Glu	Asp	Leu	Lys	Arg	
				30					35						40	

ttg	ggc	att	caa	aag	gaa	att	ttt	tac	att	agc	gtg	aat	gaa	gaa	aat	258
Leu	Gly	Ile	Gln	Lys	Glu	Ile	Phe	Tyr	Ile	Ser	Val	Asn	Glu	Glu	Asn	
			45					50					55			

gaa	aaa	gcc	ctt	ttg	aat	tgt	tac	cct	aac	gct	aaa	aat	att	gca	ggg	306
Glu	Lys	Ala	Leu	Leu	Asn	Cys	Tyr	Pro	Asn	Ala	Lys	Asn	Ile	Ala	Gly	
		60					65						70			

ttt	ttt	cat	tta	gaa	acc	gac	tat	gta	ggg	ctt	ggg	ata	gac	cgg	caa	354
Phe	Phe	His	Leu	Glu	Thr	Asp	Tyr	Val	Gly	Leu	Gly	Ile	Asp	Arg	Gln	
		75				80					85					

atg	gcg	tgt	ctg	gcg	gta	aat	aat	ggc	gtg	gtg	gtg	gat	gcc	ggg	agt	402
Met	Ala	Cys	Leu	Ala	Val	Asn	Asn	Gly	Val	Val	Val	Asp	Ala	Gly	Ser	
90					95				100						105	

gcg	att	acg	ata	gat	tta	atc	aaa	gag	ggc	aag	cat	tta	gga	ggg	tgt	450
Ala	Ile	Thr	Ile	Asp	Leu	Ile	Lys	Glu	Gly	Lys	His	Leu	Gly	Gly	Cys	
				110					115					120		

att	tta	ccc	ggt	tta	gcc	caa	tat	att	cat	gcg	tat	aaa	aaa	agc	gct	498
Ile	Leu	Pro	Gly	Leu	Ala	Gln	Tyr	Ile	His	Ala	Tyr	Lys	Lys	Ser	Ala	
			125					130						135		

aaa	att	tta	gag	caa	cct	ttc	aag	gcc	tta	gat	tct	tta	gaa	gtt	tta	546
Lys	Ile	Leu	Glu	Gln	Pro	Phe	Lys	Ala	Leu	Asp	Ser	Leu	Glu	Val	Leu	
		140					145					150				

cct	aaa	agc	act	aga	gac	gct	gtg	aat	tac	ggc	atg	gtt	ttg	agc	gtc	594
Pro	Lys	Ser	Thr	Arg	Asp	Ala	Val	Asn	Tyr	Gly	Met	Val	Leu	Ser	Val	

[illegible]

ttgttttttaa	tctttcttat	tttcattaat	tgttacgaat	agaaatactt	aaggggggttt	60
ttcattctta	aaaaaaggat	tttttaagga	aattgaatct	tgtagtctt	tgtataacaa	120
attatgtgat	aatcaccaca	agtaatcggc	ttagtgtcac	attacgaaga	ttaaatgaca	180
taaaaggaaa	aaag atg gtt aat aaa gat gtg aaa	caa acc act gct ttt				230
	Met Val Asn Lys Asp Val Lys	Gln Thr Thr Ala Phe				
	1	5	10			

ggt cct gtt tta tta caa agc act tgg ttt ttg gaa aag tta gcg gcg 326
Gly Pro Val Leu Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala
30 35 40

ttt gac aga gaa aga atc cct gaa agg gtg gtg cat gct aaa gga agc 374
Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser
45 50 55 60

gga gct tat ggc act ttc act gtg act aaa gac atc act aaa tac act 422
Gly Ala Tyr Gly Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr
65 70 75

aaa gcg aaa att ttc tct aaa gtg ggc aaa aaa acc gaa tgc ttc ttc 470
Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe
80 85 90

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aga ttt tct act gtg gct ggt gaa aga ggc agt gcg gat gcg gtg aga      518
Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg
          95                  100                  105

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gac cct aga ggt ttt gcg atg aag tat tac act gaa gaa ggt aac tgg 566
Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp
110 115 120

gat tta gtg ggg aac aac acg cct gtt ttc ttt atc cgt gat gcg atc 614
Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile
125 130 135 140

aaa ttc cct gat ttc atc cac act caa aaa cga gat cct caa acc aat 662
Lys Phe Pro Asp Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn
145 150 155

ttg cct aac cat gac atg gta tgg gat ttt tgg agt aat gtt cct gaa 710
 Leu Pro Asn His Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu
 160 165 170

agc tta tac caa gta aca tgg gtt atg agc gat agg ggt att cct aaa 758
 Ser Leu Tyr Gln Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys
 175 180 185

tct ttc cgc cac atg gat ggt ttt ggc agc cac act ttc agt ctt atc 806
Ser Phe Arg His Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile
190 195 200

<400> 80
 Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp Leu Lys Ile
 1 5 10 15
 Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys Val Val Gly
 20 25 30
 Asn Leu Ala Thr Glu Gln Pro Leu Ala Pro Lys Tyr Lys Asp His Pro
 35 40 45
 Leu Lys Gly Gly Leu Lys Asp Phe Arg Glu Cys His Leu Lys Pro Asp
 50 55 60
 Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr Leu Phe Leu
 65 70 75 80
 Val Arg Leu Gly Ser His Ser Glu Leu Phe
 85 90

<210> 81
 <211> 425
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (78)...(341)

<400> 81
 agatgtagggt aacaaagaga cagatttgat tgttgaggat ttttctagtt acagcaatga 60
 aagaaaaagg gcttttag gtg ttg aag ctc aat ctt aaa aaa tct ttt caa 110
 Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln
 1 5 10
 aaa gat ttt gat aaa ttg ctt ttg aat ggg ttt gat gat agc gtt ttg 158
 Lys Asp Phe Asp Lys Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu
 15 20 25
 aat gaa gtc att cta acc tta aga aaa aaa gaa ccg cta gat cca caa 206
 Asn Glu Val Ile Leu Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln
 30 35 40
 ttt caa gat cat gcc tta aag gga aag tgg aaa cct ttt agg gaa tgc 254
 Phe Gln Asp His Ala Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys
 45 50 55
 cac att aag cct gat gtt ttg ctt gtg tat tta gtg aaa gat gat gaa 302
 His Ile Lys Pro Asp Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu
 60 65 70 75
 ctg att ttg tta agg tta ggc agt cat agc gag ctg ttt taatccaccc 351
 Leu Ile Leu Leu Arg Leu Gly Ser His Ser Glu Leu Phe
 80 85
 acacccctta taacgcttaa accaaatcgc ttgcgctata atgaactgat attatatattt 411
 aaaaggaata aaca 425

<210> 82
 <211> 88
 <212> PRT
 <213> Helicobacter pylori

<400> 82
 Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln Lys Asp Phe Asp Lys

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1           5           10           15
Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu Asn Glu Val Ile Leu
20           25           30
Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln Phe Gln Asp His Ala
35           40           45
Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys His Ile Lys Pro Asp
50           55           60
Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu Leu Ile Leu Leu Arg
65           70           75           80
Leu Gly Ser His Ser Glu Leu Phe
85

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<210> 83
 <211> 844
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (111)...(779)

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<400> 83
gtcgttatttc gcgcttaatg agaacagagg tttttaaaac tatggtttcg tttagggttta 60
attaaatttc gctacaatta aataaaaacg ataattttag agagattggc atg caa 116
Met Gln
1

ggt tta tgg att tat cca gag gat aca gaa gtt tta ggg gtt gct tgt 164
Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val Ala Cys
5 10 15

aag agc ctt tta aaa gca cta acg cca cgc tat caa aaa gtc gcc ttg 212
Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val Ala Leu
20 25 30

ttt tcg ccc att agt gga ggg tgt gag agc ttg gag gag tgc gag agc 260
Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys Glu Ser
35 40 45 50

ttg aac cct tta gaa ttt cat agt gcg ata agc aaa caa aag gct tta 308
Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys Ala Leu
55 60 65

gag ctt gcg agc acc gct caa gaa gag tta cta ttt gaa acg att ctc 356
Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr Ile Leu
70 75 80

aaa cgc tat gat gaa tta caa tcc acg cat gat ttt gtc att aat ttg 404
Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile Asn Leu
85 90 95

ggg tgt gcg ccg aag ttt ttc tta aac gct cct tta gat tta aac acc 452
Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu Asn Thr
100 105 110

att tta gcc aag cat tta aac gct tct gtt gtg gct gtc gcg caa acg 500
Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala Gln Thr
115 120 125 130

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agt ttg gaa tat ttg aaa gcc atg cac tct cat att ctc aaa aaa gaa      548
Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys Lys Glu
              135                      140                      145

gcc cct ttc gct gta ggg tta ttt gcg ggc gaa acg ctt gaa aaa cca      596
Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu Lys Pro
              150                      155                      160

cat ttt tta agc atg tct ctt tgc aag caa caa tgc gaa tta gaa gcg      644
His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu Glu Ala
              165                      170                      175

gat ctg att gaa agc gtg ttg caa ata aaa agc gag att att acc cct      692
Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile Thr Pro
              180                      185                      190

tta gcc ttt caa agg ggt ttg gaa aaa aag gct aaa aaa cag att aaa      740
Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln Ile Lys
              195                      200                      205                      210

aaa gtg gtt tta cca gag agc gaa aag atg aaa gga ttt tgaaagctgc      789
Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe
              215                      220

acatcgtttg aatttaatgg gcgcggtagg attgatctta ttaggcgata aagaa      844

<210> 84
<211> 223
<212> PRT
<213> Helicobacter pylori

<400> 84
Met Gln Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val
 1      5      10      15
Ala Cys Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val
 20      25      30
Ala Leu Phe Ser Pro Ile Ser Gly Cys Glu Ser Leu Glu Glu Cys
 35      40      45
Glu Ser Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys
 50      55      60
Ala Leu Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr
 65      70      75      80
Ile Leu Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile
 85      90      95
Asn Leu Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu
 100     105     110
Asn Thr Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala
 115     120     125
Gln Thr Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys
 130     135     140
Lys Glu Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu
 145     150     155     160
Lys Pro His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu
 165     170     175
Glu Ala Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile
 180     185     190
Thr Pro Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln
 195     200     205
Ile Lys Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe

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210

215

220

<210> 85

<211> 821

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (79)...(753)

<400> 85

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agccagaaat tgggcaaa atg tgg aat ttt aac acc gaa tac agc agt cag 111

Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln

1

5

10

tat ttt gat ttt aga gcc gcc ggt ttt gtc caa ttg att tct aat tac 159

Tyr Phe Asp Phe Arg Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr

15

20

25

atc aat caa ttt tct tca acg ctt ttt gta acc aac ttg ccc gca caa 207

Ile Asn Gln Phe Ser Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln

30

35

40

gat att att tat gtg cct ggt tat gaa gtt tca ggg acg gct aaa tac 255

Asp Ile Ile Tyr Val Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr

45

50

55

aag ggc ttt tct tta ggc ttg agc gtg gcg cga tca tgg cct tct tta 303

Lys Gly Phe Ser Leu Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu

60

65

70

75

aag ggc cgt ttg atc gct gat gtg tat gaa ttg gcg gcc acg aca ggc 351

Lys Gly Arg Leu Ile Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly

80

85

90

aat gtg ttt att ttg acg gca agt tat aaa atc cca cgc act ggt ctt 399

Asn Val Phe Ile Leu Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu

95

100

105

agc atc act tgg ctt tca cgc ttc gtt acg gat ttg agt tat tgc tct 447

Ser Ile Thr Trp Leu Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser

110

115

120

tat agc cct tat cgt aac ggc cct acg gat att gac aga cgg cct agt 495

Tyr Ser Pro Tyr Arg Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser

125

130

135

aat tgc cct aaa acg ccc ggc att ttt cat gtt cat aaa ccc ggt tat 543

Asn Cys Pro Lys Thr Pro Gly Ile Phe His Val His Lys Pro Gly Tyr

140

145

150

155

ggg gtg agc agt ttt ttt gta acc tac aaa ccc acc tat aag aag ctt 591

Gly Val Ser Ser Phe Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu

160

165

170

aaa ggc ttg agc ttg aat gcg gtg ttt aac aat gtt ttt aac caa caa 639

Lys Gly Leu Ser Leu Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln

175	180	185	
tat att gat caa gca agc ccg gtg atg agc cct gat gaa ccc aat caa			687
Tyr Ile Asp Gln Ala Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln			
190	195	200	
gac aaa tac gca aga ggc atg gca gag cct ggc ttt aac gct aga ttt			735
Asp Lys Tyr Ala Arg Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe			
205	210	215	
gaa att tcc tat aag ttt taataatgga tctaaaaata aggatttcat			783
Glu Ile Ser Tyr Lys Phe			
220	225		
gggtagcgga tctaatacaaa aataaaacat tctttaga			821

<210> 86
 <211> 225
 <212> PRT
 <213> Helicobacter pylori

<400> 86

Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln Tyr Phe Asp Phe Arg	
1 5 10 15	
Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr Ile Asn Gln Phe Ser	
20 25 30	
Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln Asp Ile Ile Tyr Val	
35 40 45	
Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr Lys Gly Phe Ser Leu	
50 55 60	
Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu Lys Gly Arg Leu Ile	
65 70 75 80	
Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly Asn Val Phe Ile Leu	
85 90 95	
Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu Ser Ile Thr Trp Leu	
100 105 110	
Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser Tyr Ser Pro Tyr Arg	
115 120 125	
Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser Asn Cys Pro Lys Thr	
130 135 140	
Pro Gly Ile Phe His Val His Lys Pro Gly Tyr Gly Val Ser Ser Phe	
145 150 155 160	
Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu Lys Gly Leu Ser Leu	
165 170 175	
Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln Tyr Ile Asp Gln Ala	
180 185 190	
Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln Asp Lys Tyr Ala Arg	
195 200 205	
Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe Glu Ile Ser Tyr Lys	
210 215 220	
Phe	
225	

<210> 87
 <211> 1350
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS
 <222> (60)...(1202)

<400> 87

aattttgaaa acattgactc agttttcgctc tcaagggcgt ttaattcaag gatcaaagc	59
atg aat tta aat ttt atg ccc cta ttg cat gct tat aac cat gcg agc	107
Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser	
1 5 10 15	
att gat ttt cat ttc aat tct agt gct agg gat ttt tgc gtg cat gaa	155
Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu	
20 25 30	
gtg cct ttg tat gaa ttt agt aac acg ggc gaa cat gcc gtt att caa	203
Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln	
35 40 45	
gtg agg aaa agc ggt tta agc act tta gaa atg ctt cag att ttt tct	251
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser	
50 55 60	
caa att tta ggg gta aga atc gct gaa ttg ggt tat gcg ggc ttg aaa	299
Gln Ile Leu Gly Val Arg Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys	
65 70 75 80	
gat aaa aac gcg ctg acg act caa ttc atc tca ctc cct aaa aaa tac	347
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr	
85 90 95	
gcc cct tta tta gaa aaa aat acg agc aac ttt caa gaa aaa aac ctt	395
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu	
100 105 110	
aaa atc ctg tct ttg aat tac cac cac aat aaa atc aaa ttg ggg cat	443
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His	
115 120 125	
ttg aaa ggg aat cgc ttt ttt atg cgt ttt aaa aaa atg acc cct cta	491
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu	
130 135 140	
aac gct caa aaa aca aag cag gtt tta gaa caa atc gcg cag ttt gga	539
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly	
145 150 155 160	
atg cct aat tat ttt ggc tcg caa cgc ttt ggg aag ttc aat gac aac	587
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn	
165 170 175	
cac caa gag ggt tta aaa atc tta caa aat caa acg aaa ttc gcc cat	635
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His	
180 185 190	
caa aaa tta aac gct ttt tta att tca agc tat caa agt tat ttg ttt	683
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe	
195 200 205	
aac gcg ctt tta agc aaa cga tta gaa atc agt aaa atc att agc gct	731
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala	

50		55		60
Gln Ile Leu Gly Val Arg	Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys			
65	70	75	80	
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr				
	85	90	95	
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu				
	100	105	110	
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His				
	115	120	125	
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu				
	130	135	140	
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly				
	145	150	155	160
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn				
	165	170	175	
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His				
	180	185	190	
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe				
	195	200	205	
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala				
	210	215	220	
Phe Ser Val Lys Glu Asn Leu Glu Phe Phe Lys Gln Lys Asn Leu Ser				
	225	230	235	240
Val Asp Ser Asp Thr Leu Lys Thr Leu Lys Asn Gln Ala His Pro Phe				
	245	250	255	
Lys Ile Leu Glu Gly Asp Val Met Cys His Tyr Pro Tyr Gly Lys Phe				
	260	265	270	
Phe Asp Ala Leu Glu Leu Glu Lys Glu Gly Glu Arg Phe Leu Lys Lys				
	275	280	285	
Glu Val Ala Pro Thr Gly Leu Leu Asp Gly Lys Lys Ala Leu Tyr Ala				
	290	295	300	
Lys Asn Leu Ser Leu Glu Ile Glu Lys Glu Phe Gln His Asn Leu Leu				
	305	310	315	320
Ser Ser His Ala Lys Thr Leu Gly Ser Arg Arg Phe Phe Trp Val Phe				
	325	330	335	
Val Glu Asn Val Thr Ser Gln Tyr Val Lys Glu Lys Ala Gln Phe Glu				
	340	345	350	
Leu Gly Phe Tyr Leu Pro Lys Gly Ser Tyr Ala Ser Ala Leu Leu Lys				
	355	360	365	
Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp Glu Phe				
	370	375	380	

<210> 89
 <211> 1080
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (76)...(828)

<400> 89

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ccagatccct	taaaa	atg aaa	ctc ccg	gtc gtt	gag agc	111
	Met	Lys	Leu	Pro	Val	
	1		5		10	
caa ggt	gaa gga	aaa agg	ata ggc	aag ccc	agt ctt	159
Gln Gly	Glu Gly	Lys Arg	Ile Gly	Lys Pro	Ser Leu	
					Phe Leu	
					Arg Leu	

attttatgct gagcgtatcg ctgacaaccc tttagggttt atccaacgct tggatctttt 948
 gcctagtatt agcgggttcg ttcaaaaatt gcgcgagcat ggcggggaat tttttgaaat 1008
 gagagagggg aacaagctca ttgggatttg tgggcttaat cctatcaatc aaacagaagc 1068
 cgagctgtgc aa 1080

<210> 90
 <211> 251
 <212> PRT
 <213> Helicobacter pylori

<400> 90
 Met Lys Leu Pro Val Val Glu Ser Phe Phe Ser Leu Gln Gly Glu Gly
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 Lys Arg Ile Gly Lys Pro Ser Leu Phe Leu Arg Leu Gly Gly Cys Asn
 20 25 30
 Leu Ser Cys Lys Gly Phe Asn Cys Lys Thr Leu Leu Asn Asp Glu Ile
 35 40 45
 Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val His Pro Lys Phe Lys Thr
 50 55 60
 Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro Leu Ile Glu Arg Leu Glu
 65 70 75 80
 Asp Leu Ala Pro Asn Tyr Lys Asp Phe Asp Phe Ile Leu Thr Gly Gly
 85 90 95
 Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Ile Ser Val Leu Glu
 100 105 110
 His Phe Tyr Arg Gln Lys Ile Pro Leu Cys Val Glu Ser Asn Gly Ser
 115 120 125
 Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys Glu Leu His Phe Thr Leu
 130 135 140
 Ser Val Lys Leu Ser Phe Ser Leu Glu Glu Glu Ser Lys Arg Ile His
 145 150 155 160
 Leu Lys Ala Leu Gln Asn Ile Leu Asn Asn Ala Lys Ser Ala His Phe
 165 170 175
 Lys Phe Val Leu Glu Ser Gln Asn Ala Ala Gln Ser Ile Ile Glu Ile
 180 185 190
 Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys Asn Asn Glu Ile Phe Leu
 195 200 205
 Met Pro Leu Gly Thr Asn Asn Asn Glu Leu Asp Lys Asn Leu Lys Thr
 210 215 220
 Leu Ala Pro Leu Ala Ile Lys His Gly Phe Arg Leu Ser Asp Arg Leu
 225 230 235 240
 His Ile Arg Leu Trp Asp Asn Gln Lys Gly Phe
 245 250

<210> 91
 <211> 1710
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (120)...(1559)

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 gattttattc ggtgggattg tcagcatcaa gcctcattgt tcctattagc gttatttta 119
 atg gtg gtt ttt act aaa aga gtc gca ctc tcg tta ttt gtg ggc att 167
 Met Val Val Phe Thr Lys Arg Val Ala Leu Ser Leu Phe Val Gly Ile
 1 5 10 15

tta gtg agc gct gtt tta atg cat tcg tta cac ctt tcc caa ctc gta Leu Val Ser Ala Val Leu Met His Ser Leu His Leu Ser Gln Leu Val 20 25 30	215
gaa tat att tat cat aaa atc act tcc gtt ttt tac act tac gag cca Glu Tyr Ile Tyr His Lys Ile Thr Ser Val Phe Tyr Thr Tyr Glu Pro 35 40 45	263
gaa aag ggg ctt aat ttc aat ctt tcc aac ctc tat gtt ttt ggg ttt Glu Lys Gly Leu Asn Phe Asn Leu Ser Asn Leu Tyr Val Phe Gly Phe 50 55 60	311
tta atc ttt tta ggc gtc tta agc caa gtg att tta aaa tcc ggt agc Leu Ile Phe Leu Gly Val Leu Ser Gln Val Ile Leu Lys Ser Gly Ser 65 70 75 80	359
gtg caa aac ttt gtc aaa aaa gct aaa aaa tac tca aaa aac gct aaa Val Gln Asn Phe Val Lys Lys Ala Lys Lys Tyr Ser Lys Asn Ala Lys 85 90 95	407
act ccc gaa ttt atc gcc ttt ttt tca ggt atc att att ttt gta gat Thr Pro Glu Phe Ile Ala Phe Phe Ser Gly Ile Ile Ile Phe Val Asp 100 105 110	455
gat tat ttt aac gcc cta acc gtg ggg caa atc tca aag tct tta aac Asp Tyr Phe Asn Ala Leu Thr Val Gly Gln Ile Ser Lys Ser Leu Asn 115 120 125	503
gac gct cat aac tcc aca cga gag cgc ttg gct tat att ata gac tcc Asp Ala His Asn Ser Thr Arg Glu Arg Leu Ala Tyr Ile Ile Asp Ser 130 135 140	551
act tca gcg ccg gtg tgc ttg cta gtc ccc att tct agt tgg ggg gcg Thr Ser Ala Pro Val Cys Leu Leu Val Pro Ile Ser Ser Trp Gly Ala 145 150 155 160	599
tat att atg ggg atc atg aat aac gac agc tcg ccc tta tta aaa gat Tyr Ile Met Gly Ile Met Asn Asn Asp Ser Ser Pro Leu Leu Lys Asp 165 170 175	647
agt ttt tcg gtg ctt gtg caa agc tta agc agt aat tat tat gcg att Ser Phe Ser Val Leu Val Gln Ser Leu Ser Ser Asn Tyr Tyr Ala Ile 180 185 190	695
ttt gca ctc att gca gtc ttt ctc acc att tta tgg caa atc aac ctc Phe Ala Leu Ile Ala Val Phe Leu Thr Ile Leu Trp Gln Ile Asn Leu 195 200 205	743
cct agc atg aga aag tat caa aac ata ggc gtg aag gat ttt tat agc Pro Ser Met Arg Lys Tyr Gln Asn Ile Gly Val Lys Asp Phe Tyr Ser 210 215 220	791
gaa caa gaa gaa agc tct tca aaa cta gcc ccc ttg agt ttg tta ccc Glu Gln Glu Glu Ser Ser Ser Lys Leu Ala Pro Leu Ser Leu Leu Pro 225 230 235 240	839
ctt tct att tta ttg ttg att gtg tcc att tca tca ttg ctt ttt tat Leu Ser Ile Leu Leu Leu Ile Val Ser Ile Ser Ser Leu Leu Phe Tyr	887

	245	250	255	
aca gga gtg att tta aaa aac act gat gcg agt ttt tcg ctc ttt tat	Thr Gly Val Ile Leu Lys Asn Thr Asp Ala Ser Phe Ser Leu Phe Tyr	935		
	260	265	270	
gga ggg ttg ttt tcg ctc atc gtt act tat ctt tta gct tat aag ttt	Gly Gly Leu Phe Ser Leu Ile Val Thr Tyr Leu Leu Ala Tyr Lys Phe	983		
	275	280	285	
tta gaa aaa ggg agc ttt ttt aaa ctc atg ttg gat ggc ttt aag agt	Leu Glu Lys Gly Ser Phe Phe Lys Leu Met Leu Asp Gly Phe Lys Ser	1031		
	290	295	300	
gtg ggg ccg gcg ata cta gtc tta acg ctc gct tgg gct atc ggg cct	Val Gly Pro Ala Ile Leu Val Leu Thr Leu Ala Trp Ala Ile Gly Pro	1079		
	305	310	315	
gtg att aga gat gac gct caa aca ggg ctt tac ttg gct aac atc agc	Val Ile Arg Asp Asp Ala Gln Thr Gly Leu Tyr Leu Ala Asn Ile Ser	1127		
	325	330	335	
aag ggg ttt tta aat aat gga gga ggc gtg tat atg cct tta atc ttt	Lys Gly Phe Leu Asn Asn Gly Gly Gly Val Tyr Met Pro Leu Ile Phe	1175		
	340	345	350	
ttt tta atc tct ggg ttt atc gct ttt tct acc ggc aca agc tgg gga	Phe Leu Ile Ser Gly Phe Ile Ala Phe Ser Thr Gly Thr Ser Trp Gly	1223		
	355	360	365	
gcg ttt gcg atc atg ctt ccc att gga gcg ggc atg gct agt gaa agc	Ala Phe Ala Ile Met Leu Pro Ile Gly Ala Gly Met Ala Ser Glu Ser	1271		
	370	375	380	
gat att att ttg att gtt tca gcg att ctc tca ggc gcg gtt tat ggc	Asp Ile Ile Leu Ile Val Ser Ala Ile Leu Ser Gly Ala Val Tyr Gly	1319		
	385	390	395	
gat cac aca agc cct att tct gac acg act ata cta tcg gct acg ggg	Asp His Thr Ser Pro Ile Ser Asp Thr Thr Ile Leu Ser Ala Thr Gly	1367		
	405	410	415	
gca ggg tgt tcg gtg caa agc cat ttt atc acg caa ctc cct tat gcg	Ala Gly Cys Ser Val Gln Ser His Phe Ile Thr Gln Leu Pro Tyr Ala	1415		
	420	425	430	
acc att gcg atg ctt tgc agc gcg gtg agt ttg ggg gtg gca agc ttt	Thr Ile Ala Met Leu Cys Ser Ala Val Ser Leu Gly Val Ala Ser Phe	1463		
	435	440	445	
atg tat tcg cgt tcg ctc gct ctt tta atc ggt gtg gct ttg ctt gtg	Met Tyr Ser Arg Ser Leu Ala Leu Leu Ile Gly Val Ala Leu Leu Val	1511		
	450	455	460	
ggg gtg ttt tat ctt tta aaa aaa ttt tat ggt gaa aat cta aaa act	Gly Val Phe Tyr Leu Leu Lys Lys Phe Tyr Gly Glu Asn Leu Lys Thr	1559		
	465	470	475	
tgaatattga ttgaagaagc ttaaaaatcc catttttttaa aattaaaata aggtttttatc		1619		

gatccctatt tgactcaaaa agagtcttat tccattatca atcaattaa aaaggttatt
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1679
 1710

<210> 92
 <211> 480
 <212> PRT
 <213> Helicobacter pylori

<400> 92

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Leu	Val	Ser	Ala	Val	Leu	Met	His	Ser	Leu	His	Leu	Ser	Gln	Leu	Val
			20					25					30		
Glu	Tyr	Ile	Tyr	His	Lys	Ile	Thr	Ser	Val	Phe	Tyr	Thr	Tyr	Glu	Pro
		35					40					45			
Glu	Lys	Gly	Leu	Asn	Phe	Asn	Leu	Ser	Asn	Leu	Tyr	Val	Phe	Gly	Phe
	50					55					60				
Leu	Ile	Phe	Leu	Gly	Val	Leu	Ser	Gln	Val	Ile	Leu	Lys	Ser	Gly	Ser
65					70					75					80
Val	Gln	Asn	Phe	Val	Lys	Lys	Ala	Lys	Lys	Tyr	Ser	Lys	Asn	Ala	Lys
				85					90					95	
Thr	Pro	Glu	Phe	Ile	Ala	Phe	Phe	Ser	Gly	Ile	Ile	Ile	Phe	Val	Asp
			100					105						110	
Asp	Tyr	Phe	Asn	Ala	Leu	Thr	Val	Gly	Gln	Ile	Ser	Lys	Ser	Leu	Asn
		115					120					125			
Asp	Ala	His	Asn	Ser	Thr	Arg	Glu	Arg	Leu	Ala	Tyr	Ile	Ile	Asp	Ser
	130					135					140				
Thr	Ser	Ala	Pro	Val	Cys	Leu	Leu	Val	Pro	Ile	Ser	Ser	Trp	Gly	Ala
145					150					155					160
Tyr	Ile	Met	Gly	Ile	Met	Asn	Asn	Asp	Ser	Ser	Pro	Leu	Leu	Lys	Asp
			165						170					175	
Ser	Phe	Ser	Val	Leu	Val	Gln	Ser	Leu	Ser	Ser	Asn	Tyr	Tyr	Ala	Ile
			180					185					190		
Phe	Ala	Leu	Ile	Ala	Val	Phe	Leu	Thr	Ile	Leu	Trp	Gln	Ile	Asn	Leu
		195					200					205			
Pro	Ser	Met	Arg	Lys	Tyr	Gln	Asn	Ile	Gly	Val	Lys	Asp	Phe	Tyr	Ser
	210					215					220				
Glu	Gln	Glu	Glu	Ser	Ser	Ser	Lys	Leu	Ala	Pro	Leu	Ser	Leu	Leu	Pro
225					230					235					240
Leu	Ser	Ile	Leu	Leu	Ile	Val	Ser	Ile	Ser	Ser	Leu	Leu	Phe	Tyr	
			245					250					255		
Thr	Gly	Val	Ile	Leu	Lys	Asn	Thr	Asp	Ala	Ser	Phe	Ser	Leu	Phe	Tyr
			260					265					270		
Gly	Gly	Leu	Phe	Ser	Leu	Ile	Val	Thr	Tyr	Leu	Leu	Ala	Tyr	Lys	Phe
		275					280					285			
Leu	Glu	Lys	Gly	Ser	Phe	Phe	Lys	Leu	Met	Leu	Asp	Gly	Phe	Lys	Ser
	290					295					300				
Val	Gly	Pro	Ala	Ile	Leu	Val	Leu	Thr	Leu	Ala	Trp	Ala	Ile	Gly	Pro
305					310					315					320
Val	Ile	Arg	Asp	Asp	Ala	Gln	Thr	Gly	Leu	Tyr	Leu	Ala	Asn	Ile	Ser
			325						330					335	
Lys	Gly	Phe	Leu	Asn	Asn	Gly	Gly	Gly	Val	Tyr	Met	Pro	Leu	Ile	Phe
			340					345					350		
Phe	Leu	Ile	Ser	Gly	Phe	Ile	Ala	Phe	Ser	Thr	Gly	Thr	Ser	Trp	Gly
		355					360					365			
Ala	Phe	Ala	Ile	Met	Leu	Pro	Ile	Gly	Ala	Gly	Met	Ala	Ser	Glu	Ser
	370					375					380				
Asp	Ile	Ile	Leu	Ile	Val	Ser	Ala	Ile	Leu	Ser	Gly	Ala	Val	Tyr	Gly
385					390					395					400

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Asp His Thr Ser Pro Ile Ser Asp Thr Thr Ile Leu Ser Ala Thr Gly
                        405                        410                        415
Ala Gly Cys Ser Val Gln Ser His Phe Ile Thr Gln Leu Pro Tyr Ala
                        420                        425                        430
Thr Ile Ala Met Leu Cys Ser Ala Val Ser Leu Gly Val Ala Ser Phe
                        435                        440                        445
Met Tyr Ser Arg Ser Leu Ala Leu Leu Ile Gly Val Ala Leu Leu Val
                        450                        455                        460
Gly Val Phe Tyr Leu Leu Lys Lys Phe Tyr Gly Glu Asn Leu Lys Thr
465                        470                        475                        480

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<210> 93
 <211> 629
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (82)...(525)

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cattaagggtg ttttaagtta a att tcc tta tct gtt aaa cat acg gat aat      111
                        Ile Ser Leu Ser Val Lys His Thr Asp Asn
                        1                        5                        10

gtt ata tct tta agg aaa gaa aat ggg gtt agg aca cta ata agt tta      159
Val Ile Ser Leu Arg Lys Glu Asn Gly Val Arg Thr Leu Ile Ser Leu
                        15                        20                        25

ggg att ttg tta agc gtt ttg agt ggc gat gat ctg aag ttg tat tca      207
Gly Ile Leu Leu Ser Val Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser
                        30                        35                        40

aaa ctt tca gtc tat tcg gct gga agt ggg atg att ggg att gat att      255
Lys Leu Ser Val Tyr Ser Ala Gly Ser Gly Met Ile Gly Ile Asp Ile
                        45                        50                        55

gac aaa cgg aca ttt tat aag cga gcg ttc gct ttc acg atg aaa tcg      303
Asp Lys Arg Thr Phe Tyr Lys Arg Ala Phe Ala Phe Thr Met Lys Ser
60                        65                        70

ttg ttc ggt gaa aac ttg ctt ttg ttt gtc aaa tta aag cat tct gcg      351
Leu Phe Gly Glu Asn Leu Leu Leu Phe Val Lys Leu Lys His Ser Ala
75                        80                        85                        90

ttg acg agc aaa cac atg aaa ggg cct tta gaa aac cgc cat cac cat      399
Leu Thr Ser Lys His Met Lys Gly Pro Leu Glu Asn Arg His His His
95                        100                        105

tct ttc act aaa aat tat gaa aaa gcg gtt aat ggt tgt caa aag tat      447
Ser Phe Thr Lys Asn Tyr Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr
110                        115                        120

ttc cat att aaa ttg cct gaa ggc gct cct agc aac ttc aaa tca ggt      495
Phe His Ile Lys Leu Pro Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly
125                        130                        135

tca tac atg gcc act atg gtg gtg cgt ttt taaagcgtta tttgggggtat      545

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Ser Tyr Met Ala Thr Met Val Val Arg Phe
140 145

tctttaatac ccttatcgtc ttttaaaata ccatctttta aaagcacaaa tttatttttt 605
agcccttttt taaatcttct taaa 629

<210> 94
<211> 148
<212> PRT
<213> Helicobacter pylori

<400> 94
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Glu Asn Gly Val Arg Thr Leu Ile Ser Leu Gly Ile Leu Leu Ser Val
20 25 30
Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser Lys Leu Ser Val Tyr Ser
35 40 45
Ala Gly Ser Gly Met Ile Gly Ile Asp Ile Asp Lys Arg Thr Phe Tyr
50 55 60
Lys Arg Ala Phe Ala Phe Thr Met Lys Ser Leu Phe Gly Glu Asn Leu
65 70 75 80
Leu Leu Phe Val Lys Leu Lys His Ser Ala Leu Thr Ser Lys His Met
85 90 95
Lys Gly Pro Leu Glu Asn Arg His His His Ser Phe Thr Lys Asn Tyr
100 105 110
Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr Phe His Ile Lys Leu Pro
115 120 125
Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly Ser Tyr Met Ala Thr Met
130 135 140
Val Val Arg Phe
145

<210> 95
<211> 626
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (98)...(547)

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cataagactt caaagatttt ttaaagtttt aacattg atg cgt tgc gtg gtg tat 115
Met Arg Cys Val Val Tyr
1 5
tct atc gct aaa agt tcg cct tta gag tta gtg aaa atc tat caa aag 163
Ser Ile Ala Lys Ser Ser Pro Leu Glu Leu Val Lys Ile Tyr Gln Lys
10 15 20
caa tgc agg caa ttt gat tgc gag ctg gaa ttg gtg gat tta ttc cct 211
Gln Cys Arg Gln Phe Asp Cys Glu Leu Glu Leu Val Asp Leu Phe Pro
25 30 35
aaa aat acc gcc aac gct caa aaa gtt tct aaa aaa ctg gct caa aaa 259
Lys Asn Thr Ala Asn Ala Gln Lys Val Ser Lys Lys Leu Ala Gln Lys
40 45 50

agc tac tct cta gct ttt gag ccg tat tta aac cct aag gca aaa aat 307
 Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu Asn Pro Lys Ala Lys Asn
 55 60 65 70

atc gcc tta cac cct aaa gct caa agg ggc gat agc ttt gcg ttt agt 355
 Ile Ala Leu His Pro Lys Ala Gln Arg Gly Asp Ser Phe Ala Phe Ser
 75 80 85

aaa atg tta gaa aat cat ctt aat att aat ttt ttt atc gct gga gcg 403
 Lys Met Leu Glu Asn His Leu Asn Ile Asn Phe Phe Ile Ala Gly Ala
 90 95 100

tat ggg ttt gaa gaa aat ttt tta aag gat tgt caa gct tgg agt ttg 451
 Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp Cys Gln Ala Trp Ser Leu
 105 110 115

agc gag atg act ttt agc cat gaa gtg gct aaa att gtc tta tgc gag 499
 Ser Glu Met Thr Phe Ser His Glu Val Ala Lys Ile Val Leu Cys Glu
 120 125 130

caa atc tat agg gct tta agc att att ttt aag cat cca tac cat aaa 547
 Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe Lys His Pro Tyr His Lys
 135 140 145 150

taggaggtgc gcatgcgttt ttacattatc ttacattttt tgtttattgt gggtttttgg 607
 gtgtttgttt atagtattg 626

<210> 96
 <211> 150
 <212> PRT
 <213> Helicobacter pylori

<400> 96
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 20 25 30
 Leu Val Asp Leu Phe Pro Lys Asn Thr Ala Asn Ala Gln Lys Val Ser
 35 40 45
 Lys Lys Leu Ala Gln Lys Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu
 50 55 60
 Asn Pro Lys Ala Lys Asn Ile Ala Leu His Pro Lys Ala Gln Arg Gly
 65 70 75 80
 Asp Ser Phe Ala Phe Ser Lys Met Leu Glu Asn His Leu Asn Ile Asn
 85 90 95
 Phe Phe Ile Ala Gly Ala Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp
 100 105 110
 Cys Gln Ala Trp Ser Leu Ser Glu Met Thr Phe Ser His Glu Val Ala
 115 120 125
 Lys Ile Val Leu Cys Glu Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe
 130 135 140
 Lys His Pro Tyr His Lys
 145 150

<210> 97
 <211> 1053
 <212> DNA
 <213> Helicobacter pylori

Parameter	Unit	Value	Standard Error	z	P	95% CI
Intercept		1.00	0.00			
Age	Year	0.02	0.01	1.50	0.13	-0.01, 0.05
Gender						
Male		0.01	0.02	0.40	0.69	-0.03, 0.05
Female		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Marital status						
Married		0.01	0.02	0.40	0.69	-0.03, 0.05
Single		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Education	Year	0.01	0.01	1.00	0.32	-0.01, 0.03
Income	Year	0.01	0.01	1.00	0.32	-0.01, 0.03
Health status						
Good		0.01	0.02	0.40	0.69	-0.03, 0.05
Poor		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living alone		0.01	0.02	0.40	0.69	-0.03, 0.05
Living with family		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a nursing home		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a community		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a hospital		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a long-term care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a residential care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a nursing home		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a community		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a hospital		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a long-term care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a residential care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a nursing home		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a community		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a hospital		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a long-term care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a residential care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a nursing home		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a community		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a hospital		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a long-term care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a residential care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a nursing home		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a community		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a hospital		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a long-term care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a residential care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a nursing home		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a community		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a hospital		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a long-term care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a residential care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a nursing home		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a community		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a hospital		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a long-term care facility		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a residential care facility		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a nursing home		-0.01	0.02	-0.40	0.69	-0.05, 0.03
Living in a community		0.01	0.02	0.40	0.69	-0.03, 0.05
Living in a hospital		-0.01	0.02	-0.40	0.69</	

-106-

210		215		220
Pro Gly Ala Met Ile Gly Phe Ala Gly Pro Arg Val Ile Lys Gln Thr				
225		230		235
Ile Gly Ala Asp Leu Pro Glu Gly Phe Gln Thr Ala Glu Phe Leu Leu				240
	245		250	255
Glu His Gly Leu Ile Asp Met Ile Val His Arg Lys Asp Leu Lys Lys				
	260		265	270
Thr Leu Ser Asp Leu Ile Ala Met Met Thr His Lys Thr Ser Lys Ile				
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Phe				

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 <212> DNA
 <213> Helicobacter pylori

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gcttataata aacaaaatta gcttaagagt agtg atg caa ggg ttt ctt tta caa	115
Met Gln Gly Phe Leu Leu Gln	
1 5	
aca caa agc ata aga gat gaa gat ttg atc gtg cgc gtt tta acc aaa	163
Thr Gln Ser Ile Arg Asp Glu Asp Leu Ile Val Arg Val Leu Thr Lys	
10 15 20	
aac cag ctc aaa acc ctc tat cgt ttc tat ggc aaa cgc cat agc gtg	211
Asn Gln Leu Lys Thr Leu Tyr Arg Phe Tyr Gly Lys Arg His Ser Val	
25 30 35	
ctg aat gtg ggg cgt aaa att gat ttt gaa gaa gaa aac gat gat aag	259
Leu Asn Val Gly Arg Lys Ile Asp Phe Glu Glu Glu Asn Asp Asp Lys	
40 45 50 55	
ttt tta ccc aag tta agg aat att ttg cat tta ggc tat att tgg gaa	307
Phe Leu Pro Lys Leu Arg Asn Ile Leu His Leu Gly Tyr Ile Trp Glu	
60 65 70	
aga gaa atg gag cgc ttg ttt ttt tgg caa cgc ttt tgc gct ctc ttg	355
Arg Glu Met Glu Arg Leu Phe Phe Trp Gln Arg Phe Cys Ala Leu Leu	
75 80 85	
ttt agg cat tta gaa ggc gtg cat tct tta gat agc gtc tat ttt gac	403
Phe Arg His Leu Glu Gly Val His Ser Leu Asp Ser Val Tyr Phe Asp	
90 95 100	
act tta gat gat ggg gct aac aaa ctc gcc aaa cag cac ccc tta aga	451
Thr Leu Asp Asp Gly Ala Asn Lys Leu Ala Lys Gln His Pro Leu Arg	
105 110 115	
gtg att tta gaa atg tat gca acg ctt ttg aat ttt gaa ggg cgc ttg	499
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<213> Helicobacter pylori

<220>

<221> CDS

<222> (76)...(927)

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Met Asn Ala Trp Asn Thr Ile Tyr Asp Gln Phe Asn
1 5 10

cct atc gct ttt agt ctt ggc agt att gaa gtg cat tgg tat ggt ttg 159
Pro Ile Ala Phe Ser Leu Gly Ser Ile Glu Val His Trp Tyr Gly Leu
15 20 25

gcg tat gcg tgt gcg att gtt acc gct ttt tat atg gcg tta aga atg 207
Ala Tyr Ala Cys Ala Ile Val Thr Ala Phe Tyr Met Ala Leu Arg Met
30 35 40

atc caa aaa gac ccc aag cga ttc ccc att gaa agg aag gaa ttt gag 255
Ile Gln Lys Asp Pro Lys Arg Phe Pro Ile Glu Arg Lys Glu Phe Glu
45 50 55 60

agt tat ttt tta tgg gcg gag ctt ggc att gtg cta ggg gca agg ata 303
Ser Tyr Phe Leu Trp Ala Glu Leu Gly Ile Val Leu Gly Ala Arg Ile
65 70 75

gga tac att ctt att tat gag cct aat tct ggc tat tat ttg acg cat 351
Gly Tyr Ile Leu Ile Tyr Glu Pro Asn Ser Gly Tyr Tyr Leu Thr His
80 85 90

ttt tgg caa atc ttt aac cct ttt gat agc cat ggg aat ttt gta ggc 399
Phe Trp Gln Ile Phe Asn Pro Phe Asp Ser His Gly Asn Phe Val Gly
95 100 105

att cgt ggg atg agc tat cat ggg ggg ttg gtg ggg ttt ttg atc gct 447
Ile Arg Gly Met Ser Tyr His Gly Gly Leu Val Gly Phe Leu Ile Ala
110 115 120

tcg tat ctt tat agc cgt aag gat ttg aaa aag ctt ttg att tat ttg 495
Ser Tyr Leu Tyr Ser Arg Lys Asp Leu Lys Lys Leu Leu Ile Tyr Leu
125 130 135 140

gat ttg att gcg atc agc ctg cct tta ggg tat gtt ttt ggg agg att 543
Asp Leu Ile Ala Ile Ser Leu Pro Leu Gly Tyr Val Phe Gly Arg Ile
145 150 155

ggg aat ttt tta aac cag gag ctt gtg gga aga att gtc ccc aaa gac 591
Gly Asn Phe Leu Asn Gln Glu Leu Val Gly Arg Ile Val Pro Lys Asp
160 165 170

agc cat tta ggg caa atc ata ggc att atg gtg gat aat gag ttg cgt 639
Ser His Leu Gly Gln Ile Ile Gly Ile Met Val Asp Asn Glu Leu Arg
175 180 185

tat ccc agc caa ttg att gaa gcg ttt tta gag ggg gtt atc gtg ttt 687
Tyr Pro Ser Gln Leu Ile Glu Ala Phe Leu Glu Gly Val Ile Val Phe
190 195 200

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Pro	Asp	Ser	Gln	Met	Gly	Val	Tyr	Phe	Leu	Asn	Leu	Ser	Met	Gly	Gln			
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Ile	Leu	Ser	Leu	Phe	Met	Val	Ile	Val	Ser	Leu	Gly	Ile	Leu	Leu	Tyr			
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			1				5									
aaa	cta	caa	gag	tat	tgg	aag	aat	caa	ggc	tgt	ttg	gtg	atc	cag	cct	160
Lys	Leu	Gln	Glu	Tyr	Trp	Lys	Asn	Gln	Gly	Cys	Leu	Val	Ile	Gln	Pro	
10					15					20					25	
tat	gat	att	cct	gca	gga	gct	ggg	aca	ttc	cat	ccg	gcc	acg	ctt	tta	208
Tyr	Asp	Ile	Pro	Ala	Gly	Ala	Gly	Thr	Phe	His	Pro	Ala	Thr	Leu	Leu	
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agg	agt	ttg	gat	aaa	aag	ccg	tgg	aat	gtg	gcg	tat	gtc	gcg	ccc	tct	256
Arg	Ser	Leu	Asp	Lys	Lys	Pro	Trp	Asn	Val	Ala	Tyr	Val	Ala	Pro	Ser	
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Arg	Arg	Pro	Thr	Asp	Gly	Arg	Tyr	Gly	Glu	Asn	Pro	Asn	Arg	Leu	Gly	
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agt	tat	tac	caa	ttc	caa	gta	gtc	atc	aag	ccc	agc	cct	tct	aat	atc	352
Ser	Tyr	Tyr	Gln	Phe	Gln	Val	Val	Ile	Lys	Pro	Ser	Pro	Ser	Asn	Ile	
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Gln	Glu	Leu	Tyr	Leu	Lys	Ser	Leu	Glu	Val	Leu	Gly	Ile	Asn	Leu	Asn	
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gag	cat	gat	ata	cga	ttt	gta	gaa	gac	aat	tgg	gag	agt	ccg	act	tta	448
Glu	His	Asp	Ile	Arg	Phe	Val	Glu	Asp	Asn	Trp	Glu	Ser	Pro	Thr	Leu	
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Gly	Ala	Trp	Gly	Leu	Gly	Trp	Glu	Val	Trp	Leu	Asp	Gly	Met	Glu	Val	
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Thr	Gln	Phe	Thr	Tyr	Phe	Gln	Gln	Val	Gly	Gly	Ile	Ala	Cys	Ser	Pro	
	140						145					150				

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155160165																
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170175180185																
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190200																
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220225230																
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235240245																
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250255260265																
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270275280																
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285290295																
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Ala Glu Asn Gly Val Ser																
300																
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<212> PRT
<213> Helicobacter pylori
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			20					25					30		
Gly	Thr	Phe	His	Pro	Ala	Thr	Leu	Leu	Arg	Ser	Leu	Asp	Lys	Lys	Pro
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Trp	Asn	Val	Ala	Tyr	Val	Ala	Pro	Ser	Arg	Arg	Pro	Thr	Asp	Gly	Arg
	50				55						60				
Tyr	Gly	Glu	Asn	Pro	Asn	Arg	Leu	Gly	Ser	Tyr	Tyr	Gln	Phe	Gln	Val
65				70						75				80	

Val	Ile	Lys	Pro	Ser 85	Pro	Ser	Asn	Ile	Gln 90	Glu	Leu	Tyr	Leu	Lys 95	Ser
Leu	Glu	Val	Leu	Gly	Ile	Asn	Leu	Asn 105	Glu	His	Asp	Ile	Arg 110	Phe	Val
Glu	Asp	Asn	Trp	Glu	Ser	Pro	Thr 120	Leu	Gly	Ala	Trp	Gly 125	Leu	Gly	Trp
Glu	Val	Trp	Leu	Asp	Gly	Met 135	Glu	Val	Thr	Gln	Phe 140	Thr	Tyr	Phe	Gln
Gln	Val	Gly	Gly	Ile	Ala 150	Cys	Ser	Pro	Ile	Pro 155	Val	Glu	Ile	Thr	Tyr
145	Gly	Leu	Glu	Arg	Leu 165	Ala	Met	Tyr	Val	Gln 170	Lys	Val	Glu	Asn 175	Ile
Glu	Ile	Glu	Trp	Ala	Lys	Lys	Asn	His 185	Asp	Ser	Val	Asn	Tyr 190	Ala	Gln
Val	His	Leu	Glu	Ser	Glu	Tyr	Glu 200	Phe	Ser	Lys	Tyr	His 205	Phe	Glu	Thr
Ala	Ser	Val	Lys	Arg	Leu	Leu 215	Glu	Met	Phe	Lys	Asn 220	Ala	Gln	Ala	Glu
Ala	Leu	His	Cys	Leu	Glu 230	Asn	Lys	Leu	Pro	Leu 235	Pro	Ala	Tyr	Asp	Phe
225	Val	Met	Leu	Cys	Ser 245	His	Phe	Phe	Asn	Ile 250	Leu	Asp	Ala	Arg	Lys
Ile	Ser	Val	Ala	Glu	Arg	Gln	Asn	Tyr 265	Ile	Leu	Gln	Ile	Arg 270	Asp	Leu
Ala	Lys	Gly	Cys	Ala	Leu	Leu	Tyr 280	Lys	Glu	Gln	Glu	Glu 285	Glu	Arg	Glu
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Met	Ala	Gln	Lys	Thr	Leu	Leu	Ile	Ile	Thr	Asp	Gly	Ile	Gly	Tyr			
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cgt	aaa	gat	agc	gat	cat	aac	gct	ttc	ttc	cat	gcc	aaa	aaa	ccc	act		158
Arg	Lys	Asp	Ser	Asp	His	Asn	Ala	Phe	Phe	His	Ala	Lys	Lys	Pro	Thr		
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tat	gat	ttg	atg	ttt	aaa	acc	ttg	cct	tat	agc	ctg	att	gat	acg	cat		206
Tyr	Asp	Leu	Met	Phe	Lys	Thr	Leu	Pro	Tyr	Ser	Leu	Ile	Asp	Thr	His		
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Gly	Leu	Ser	Val	Gly	Leu	Pro	Lys	Gly	Gln	Met	Gly	Asn	Ser	Glu	Val		
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ggg	cat	atg	tgt	att	ggg	gct	ggt	agg	gtg	ctc	tat	cag	gat	tta	gtc		302
Gly	His	Met	Cys	Ile	Gly	Ala	Gly	Arg	Val	Leu	Tyr	Gln	Asp	Leu	Val		
65						70					75						

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80 85 90 95	
ttt tta aac acg atc caa aaa agc cct gtg gtg cat ctt atg ggt tta	398
Phe Leu Asn Thr Ile Gln Lys Ser Pro Val Val His Leu Met Gly Leu	
100 105 110	
atg agc gat gga ggc gtg cat tca cac att gag cat ttt atc gct ctg	446
Met Ser Asp Gly Gly Val His Ser His Ile Glu His Phe Ile Ala Leu	
115 120 125	
gct tta gag tgt gaa aaa tcc cat aaa aaa gtc tgt ctg cat tta atc	494
Ala Leu Glu Cys Glu Lys Ser His Lys Lys Val Cys Leu His Leu Ile	
130 135 140	
acc gat ggg cgc gat gtc gct cct aaa agc gct tta act tat tta aaa	542
Thr Asp Gly Arg Asp Val Ala Pro Lys Ser Ala Leu Thr Tyr Leu Lys	
145 150 155	
caa atg caa aat atc tgc aat gaa agc att caa atc gct acc ata agc	590
Gln Met Gln Asn Ile Cys Asn Glu Ser Ile Gln Ile Ala Thr Ile Ser	
160 165 170 175	
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Gly Arg Phe Tyr Ala Met Asp Arg Asp Lys Arg Phe Glu Arg Ile Glu	
180 185 190	
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Leu Ala Tyr His Ser Leu Met Gly Leu Asn His Thr Pro Leu Ser Pro	
195 200 205	
agc gag tat atc caa agc cag tat gat aaa aat atc acc gat gaa ttt	734
Ser Glu Tyr Ile Gln Ser Gln Tyr Asp Lys Asn Ile Thr Asp Glu Phe	
210 215 220	
atc atg ccc gct tgt ttt aaa aat tat tgc ggc atg caa gat gat gag	782
Ile Met Pro Ala Cys Phe Lys Asn Tyr Cys Gly Met Gln Asp Asp Glu	
225 230 235	
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Ser Phe Ile Phe Ile Asn Phe Arg Asn Asp Arg Ala Arg Glu Ile Val	
240 245 250 255	
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Ser Ala Leu Gly Gln Lys Gln Phe Ser Gly Phe Lys Arg Gln Val Phe	
260 265 270	
aaa aaa ctc cat atc gct acc atg acg cct tat gat aac act ttc ccc	926
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275 280 285	
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Tyr Pro Val Leu Phe Pro Lys Glu Ser Val Gln Asn Thr Leu Ala Glu	
290 295 300	
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Val Val Ser Gln His Asn Leu Thr Gln Ser His Ile Ala Glu Thr Glu	

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Ala	Val	Glu	Ala	Val	Asp	Ala	Cys	Leu	Gly	Glu	Ile	Leu	Ser	Leu	Ala																		
400											405											410											415
aaa	aaa	ttg	gat	tac	gcc	atg	ctt	tta	acc	agc	gat	cat	ggg	aat	tgc		1358																
Lys	Lys	Leu	Asp	Tyr	Ala	Met	Leu	Leu	Thr	Ser	Asp	His	Gly	Asn	Cys																		
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Glu	Arg	Met	Lys	Asp	Glu	Asn	Gln	Asn	Pro	Leu	Thr	Asn	His	Thr	Ala																		
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Gly	Ser	Val	Tyr	Cys	Phe	Val	Leu	Gly	Asp	Gly	Val	Lys	Ser	Ile	Lys																		
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aac	gga	gcc	tta	aac	aat	atc	gct	agc	agc	gtg	tta	aaa	ctc	atg	ggc		1502																
Asn	Gly	Ala	Leu	Asn	Asn	Ile	Ala	Ser	Ser	Val	Leu	Lys	Leu	Met	Gly																		
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Leu	Lys	Ala	Pro	Ala	Thr	Met	Asp	Glu	Pro	Leu	Phe																						
480											485											490											
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Lys	Asp	Ser	Asp	His	Asn	Ala	Phe	Phe	His	Ala	Lys	Lys	Pro	Thr	Tyr																		
				20											25											30							

Asp	Leu	Met	Phe	Lys	Thr	Leu	Pro	Tyr	Ser	Leu	Ile	Asp	Thr	His	Gly
		35					40					45			
Leu	Ser	Val	Gly	Leu	Pro	Lys	Gly	Gln	Met	Gly	Asn	Ser	Glu	Val	Gly
	50					55					60				
His	Met	Cys	Ile	Gly	Ala	Gly	Arg	Val	Leu	Tyr	Gln	Asp	Leu	Val	Lys
65					70					75					80
Ile	Ser	Leu	Ser	Leu	Gln	Asn	Asp	Glu	Leu	Lys	Asn	Asn	Pro	Ala	Phe
				85				90						95	
Leu	Asn	Thr	Ile	Gln	Lys	Ser	Pro	Val	Val	His	Leu	Met	Gly	Leu	Met
			100					105					110		
Ser	Asp	Gly	Gly	Val	His	Ser	His	Ile	Glu	His	Phe	Ile	Ala	Leu	Ala
		115					120					125			
Leu	Glu	Cys	Glu	Lys	Ser	His	Lys	Lys	Val	Cys	Leu	His	Leu	Ile	Thr
	130					135					140				
Asp	Gly	Arg	Asp	Val	Ala	Pro	Lys	Ser	Ala	Leu	Thr	Tyr	Leu	Lys	Gln
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Met	Gln	Asn	Ile	Cys	Asn	Glu	Ser	Ile	Gln	Ile	Ala	Thr	Ile	Ser	Gly
				165					170					175	
Arg	Phe	Tyr	Ala	Met	Asp	Arg	Asp	Lys	Arg	Phe	Glu	Arg	Ile	Glu	Leu
			180					185						190	
Ala	Tyr	His	Ser	Leu	Met	Gly	Leu	Asn	His	Thr	Pro	Leu	Ser	Pro	Ser
		195					200					205			
Glu	Tyr	Ile	Gln	Ser	Gln	Tyr	Asp	Lys	Asn	Ile	Thr	Asp	Glu	Phe	Ile
	210					215					220				
Met	Pro	Ala	Cys	Phe	Lys	Asn	Tyr	Cys	Gly	Met	Gln	Asp	Asp	Glu	Ser
225					230					235					240
Phe	Ile	Phe	Ile	Asn	Phe	Arg	Asn	Asp	Arg	Ala	Arg	Glu	Ile	Val	Ser
				245					250					255	
Ala	Leu	Gly	Gln	Lys	Gln	Phe	Ser	Gly	Phe	Lys	Arg	Gln	Val	Phe	Lys
			260					265					270		
Lys	Leu	His	Ile	Ala	Thr	Met	Thr	Pro	Tyr	Asp	Asn	Thr	Phe	Pro	Tyr
		275					280					285			
Pro	Val	Leu	Phe	Pro	Lys	Glu	Ser	Val	Gln	Asn	Thr	Leu	Ala	Glu	Val
	290					295					300				
Val	Ser	Gln	His	Asn	Leu	Thr	Gln	Ser	His	Ile	Ala	Glu	Thr	Glu	Lys
305					310					315					320
Tyr	Ala	His	Val	Thr	Phe	Phe	Ile	Asn	Gly	Gly	Val	Glu	Thr	Pro	Phe
				325					330					335	
Lys	Asn	Glu	Asn	Arg	Val	Leu	Ile	Gln	Ser	Pro	Lys	Val	Thr	Thr	Tyr
			340					345					350		
Asp	Leu	Lys	Pro	Glu	Met	Ser	Ala	Lys	Glu	Val	Thr	Leu	Ala	Val	Leu
		355					360					365			
Glu	Gln	Met	Lys	Leu	Gly	Thr	Asp	Leu	Ile	Ile	Val	Asn	Phe	Ala	Asn
	370					375					380				
Gly	Asp	Met	Val	Gly	His	Thr	Gly	Asn	Phe	Glu	Ala	Ser	Val	Lys	Ala
385					390					395					400
Val	Glu	Ala	Val	Asp	Ala	Cys	Leu	Gly	Glu	Ile	Leu	Ser	Leu	Ala	Lys
				405					410					415	
Lys	Leu	Asp	Tyr	Ala	Met	Leu	Leu	Thr	Ser	Asp	His	Gly	Asn	Cys	Glu
			420					425					430		
Arg	Met	Lys	Asp	Glu	Asn	Gln	Asn	Pro	Leu	Thr	Asn	His	Thr	Ala	Gly
			435				440						445		
Ser	Val	Tyr	Cys	Phe	Val	Leu	Gly	Asp	Gly	Val	Lys	Ser	Ile	Lys	Asn
	450					455					460				
Gly	Ala	Leu	Asn	Asn	Ile	Ala	Ser	Ser	Val	Leu	Lys	Leu	Met	Gly	Leu
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Lys	Ala	Pro	Ala	Thr	Met	Asp	Glu	Pro	Leu	Phe					
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<220>
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Met Asn Phe Gln Glu Asn Leu Ala Ala Leu Asp Leu Glu	
1 5 10	
tat ctt tgg cac cct tgt tcg caa atg caa gag cat caa aat ttc ccc	158
Tyr Leu Trp His Pro Cys Ser Gln Met Gln Glu His Gln Asn Phe Pro	
15 20 25	
att atc ccc att aaa aag gct caa ggg att tac ctc tat gat ttt aat	206
Ile Ile Pro Ile Lys Lys Ala Gln Gly Ile Tyr Leu Tyr Asp Phe Asn	
30 35 40 45	
gat aac gct tac atg gat ttg atc agc tca tgg tgg gtg aat ctt ttt	254
Asp Asn Ala Tyr Met Asp Leu Ile Ser Ser Trp Trp Val Asn Leu Phe	
50 55 60	
ggg cat aat aac gcc tac atc agc cag caa ctc aaa aat caa att gat	302
Gly His Asn Asn Ala Tyr Ile Ser Gln Gln Leu Lys Asn Gln Ile Asp	
65 70 75	
gat tta gag cat gtc ctt ttg gct tct ttt agc cat aag ccc att atc	350
Asp Leu Glu His Val Leu Leu Ala Ser Phe Ser His Lys Pro Ile Ile	
80 85 90	
acg ctc tct caa agg ctt tgc cag ctc act cat atg gat aaa tgc ttt	398
Thr Leu Ser Gln Arg Leu Cys Gln Leu Thr His Met Asp Lys Cys Phe	
95 100 105	
tat gcg gat aac ggc tca tct tgt gtt gaa atc gct ttg aaa atg agc	446
Tyr Ala Asp Asn Gly Ser Ser Cys Val Glu Ile Ala Leu Lys Met Ser	
110 115 120 125	
tat cac gcc cat ttt tta aag aat caa acg cgc cgc aaa aag ctt ttt	494
Tyr His Ala His Phe Leu Lys Asn Gln Thr Arg Arg Lys Lys Leu Phe	
130 135 140	
tta tcg ctc tct aat tcc tat cat ggc gag act ttg gga gcg tta agc	542
Leu Ser Leu Ser Asn Ser Tyr His Gly Glu Thr Leu Gly Ala Leu Ser	
145 150 155	
gtg ggc gat gtg aaa ctt tat aaa gac act tac acc cct tta ttg ctc	590
Val Gly Asp Val Lys Leu Tyr Lys Asp Thr Tyr Thr Pro Leu Leu Leu	
160 165 170	
aaa aat ctc acc aca cct gtg cct aaa aac gac cat gaa ata gaa aat	638
Lys Asn Leu Thr Thr Pro Val Pro Lys Asn Asp His Glu Ile Glu Asn	
175 180 185	

agt ttg aac gct tta aag cgt ttg tta gac aag cat agt gaa gaa att Ser Leu Asn Ala Leu Lys Arg Leu Leu Asp Lys His Ser Glu Glu Ile 190 195 200 205	686
tgc gct ttc att gca gag cct ctt ttg caa tgc gca ggg aat atg cat Cys Ala Phe Ile Ala Glu Pro Leu Leu Gln Cys Ala Gly Asn Met His 210 215 220	734
att tat agc gca aga tat tta aaa caa gcc gtt tta ttg tgc aag caa Ile Tyr Ser Ala Arg Tyr Leu Lys Gln Ala Val Leu Leu Cys Lys Gln 225 230 235	782
aaa aac atc cac att att ttt gat gaa atc gct acc ggg ttt ggg cgc Lys Asn Ile His Ile Ile Phe Asp Glu Ile Ala Thr Gly Phe Gly Arg 240 245 250	830
aca ggg agc atg ttt gct tat gaa caa tgc gaa att aag ccg gat ttt Thr Gly Ser Met Phe Ala Tyr Glu Gln Cys Glu Ile Lys Pro Asp Phe 255 260 265	878
tta tgc ttg tct aag ggg att agt ggg ggg tat ttg cct tta agc gca Leu Cys Leu Ser Lys Gly Ile Ser Gly Gly Tyr Leu Pro Leu Ser Ala 270 275 280 285	926
cta tta acc cat aat gaa atc tat aac caa ttt tac gcc ccc tat gaa Leu Leu Thr His Asn Glu Ile Tyr Asn Gln Phe Tyr Ala Pro Tyr Glu 290 295 300	974
gaa aat aaa gcg ttt ttg cat tcg cac agc tac aca gga aac gct ttg Glu Asn Lys Ala Phe Leu His Ser His Ser Tyr Thr Gly Asn Ala Leu 305 310 315	1022
gca tgc gca tgc gcg aac gct acg ctg gat att ttt gaa aaa gaa aat Ala Cys Ala Cys Ala Asn Ala Thr Leu Asp Ile Phe Glu Lys Glu Asn 320 325 330	1070
gtt att gaa aag aac aag gct tta agc ggg ttt att ttt aat acg ctc Val Ile Glu Lys Asn Lys Ala Leu Ser Gly Phe Ile Phe Asn Thr Leu 335 340 345	1118
caa aac gca tta aaa ccc ttg atg gag caa caa gtg gtg tct gat tta Gln Asn Ala Leu Lys Pro Leu Met Glu Gln Gln Val Val Ser Asp Leu 350 355 360 365	1166
agg cat ttg ggc atg gtc ttt gcc ttt gaa gtc ttt att caa acc aaa Arg His Leu Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys 370 375 380	1214
gag cgt ttg agt ttg gcg gtt ttt aaa aaa act cta aaa aaa ggc ctg Glu Arg Leu Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu 385 390 395	1262
tta tta cgc cct tta aac aac acc att tac ctc atg ccc cct tac att Leu Leu Arg Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Pro Tyr Ile 400 405 410	1310
atc acg cat gaa gaa gtc aaa aag gcg gtt gcg ggg cta gtg gaa att Ile Thr His Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile 415 420 425	1358

1409

1440

<400> 108

20

35

0

100
700 gms day

115
The Low Lye

sn Ser Tyr

vs Leu Tyr

hr Pro Val

eu Lys Arg

1a Glu Proc

rg Tyr Leu

Ile Ile Phe

ne Ala Tyr

ys Gly Ile
275

SH GU THE
00

the Dea HHS

14 1511 1110

340

355

1440

Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys Glu Arg Leu
 370 375 380
 Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu Leu Leu Arg
 385 390 395 400
 Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Pro Tyr Ile Ile Thr His
 405 410 415
 Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile Leu Asp Glu
 420 425 430
 Leu Arg Lys Gly
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 Met Gly Lys Met Lys Gln Glu Thr Ala Ile
 1 5 10
 gac tat gaa aaa tta gcg aat cat tgg aat aat aat gat gaa aac agc 159
 Asp Tyr Glu Lys Leu Ala Asn His Trp Asn Asn Asn Asp Glu Asn Ser 25
 15 20 25
 gaa gca cta aac gct ttt gca gac gct tac ctt tat aaa cat gag aaa 207
 Glu Ala Leu Asn Ala Phe Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys 40
 30 35 40
 aag agt caa aag att cgg gca ata gag ata agt tct cta aac aaa gcc 255
 Lys Ser Gln Lys Ile Arg Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala 55
 45 50 55
 tgc atg gga gaa ttt tac cac aaa aac cca aaa tta ttt taataacgat 304
 Cys Met Gly Glu Phe Tyr His Lys Asn Pro Lys Leu Phe 70
 60 65 70
 cgctccaagg aaccaacgcc ccatgacctc aagaaaagag aatagcttga atcggt 360

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 <211> 71
 <212> PRT
 <213> Helicobacter pylori

<400> 110

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 Asn His Trp Asn Asn Asn Asp Glu Asn Ser Glu Ala Leu Asn Ala Phe
 20 25 30
 Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys Lys Ser Gln Lys Ile Arg
 35 40 45
 Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala Cys Met Gly Glu Phe Tyr
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 His Lys Asn Pro Lys Leu Phe

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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (62)...(1255)

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Arg His Arg Asn Arg Ala Arg Cys Thr Arg Lys Gln Ala Arg Asn Asn	
1 5 10 15	
aag agt ttt agg cat gaa aac tat ttt tat aaa gtt ttg ggt agt gca	157
Lys Ser Phe Arg His Glu Asn Tyr Phe Tyr Lys Val Leu Gly Ser Ala	
20 25 30	
act tct caa ata gaa agt ttg aaa aaa aga gaa aat gcc cta ttt gat	205
Thr Ser Gln Ile Glu Ser Leu Lys Lys Arg Glu Asn Ala Leu Phe Asp	
35 40 45	
cat tta gat agt cta aaa agt tta tta gaa aaa aca cat tgg gaa aaa	253
His Leu Asp Ser Leu Lys Ser Leu Leu Glu Lys Thr His Trp Glu Lys	
50 55 60	
gaa aaa ttc acg ccc cca ata aat gaa aaa gaa ctt aat agg caa ctt	301
Glu Lys Phe Thr Pro Pro Ile Asn Glu Lys Glu Leu Asn Arg Gln Leu	
65 70 75 80	
aaa gaa gtg aga tgg ttc aat aaa gaa act cca act tct aaa aac act	349
Lys Glu Val Arg Trp Phe Asn Lys Glu Thr Pro Thr Ser Lys Asn Thr	
85 90 95	
tat aag aaa att caa aaa tta gct gtt tat aaa agc cct tta ata aaa	397
Tyr Lys Lys Ile Gln Lys Leu Ala Val Tyr Lys Ser Pro Leu Ile Lys	
100 105 110	
gat tat ctt tat acc att aaa aaa ctt ttt gcc aca caa aaa aag att	445
Asp Tyr Leu Tyr Thr Ile Lys Lys Leu Phe Ala Thr Gln Lys Lys Ile	
115 120 125	
ata gat tta gaa aaa aat tat aaa gat tta aga gcc tta aag gaa gaa	493
Ile Asp Leu Glu Lys Asn Tyr Lys Asp Leu Arg Ala Leu Lys Glu Glu	
130 135 140	
ttt agc aaa gat tta gaa act gat tta tcc cat tca aaa aaa cgc ttt	541
Phe Ser Lys Asp Leu Glu Thr Asp Leu Ser His Ser Lys Lys Arg Phe	
145 150 155 160	
gaa ctt tac act aga cta aag agc atg agc aaa gtt ttt ata agc aaa	589
Glu Leu Tyr Thr Arg Leu Lys Ser Met Ser Lys Val Phe Ile Ser Lys	
165 170 175	
agc att gtt aaa aat tta gaa aaa att gct tta gat ttt aaa agc gat	637
Ser Ile Val Lys Asn Leu Glu Lys Ile Ala Leu Asp Phe Lys Ser Asp	

180					185					190						
aga	cat	agt	att	tcg	caa	aga	gct	ttt	gaa	ttt	ttt	aag	tat	atg	aat	685
Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn	
		195					200					205				
tat	caa	aat	tta	agc	ttg	act	gat	aaa	ggc	aat	atg	ttt	tta	gtg	gct	733
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala	
	210					215					220					
aag	ttt	ttt	aaa	gat	agt	gct	tta	ctt	ggt	aat	att	gct	agg	ttt	gaa	781
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu	
225					230					235					240	
atg	aaa	aag	ata	gat	gat	agt	gtt	aaa	aat	tct	aac	cca	caa	gac	aat	829
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn	
				245					250					255		
tta	tta	gac	aaa	caa	gtt	tgg	ctc	aat	ctt	tta	gag	cat	tta	aaa	aga	877
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg	
			260					265					270			
ctt	gaa	gag	gaa	aat	tat	tgt	ttt	gct	aag	aaa	cga	aaa	gaa	ttc	tta	925
Leu	Glu	Glu	Glu	Asn	Tyr	Cys	Phe	Ala	Lys	Lys	Arg	Lys	Glu	Phe	Leu	
		275					280					285				
gag	act	aga	gcg	atg	gag	cta	tca	aaa	gat	tta	aaa	ttt	tta	aca	cag	973
Glu	Thr	Arg	Ala	Met	Glu	Leu	Ser	Lys	Asp	Leu	Lys	Phe	Leu	Thr	Gln	
	290					295					300					
gct	aat	gaa	aat	gat	ttg	ccc	att	tat	gaa	aga	ggg	caa	agg	gat	aaa	1021
Ala	Asn	Glu	Asn	Asp	Leu	Pro	Ile	Tyr	Glu	Arg	Gly	Gln	Arg	Asp	Lys	
305					310					315					320	
atc	att	aaa	cgc	tgt	gaa	aaa	tcg	ctt	aac	ttt	ttg	cag	aaa	gaa	tta	1069
Ile	Ile	Lys	Arg	Cys	Glu	Lys	Ser	Leu	Asn	Phe	Leu	Gln	Lys	Glu	Leu	
				325					330					335		
caa	tgc	ttt	aaa	acc	tta	ttg	aaa	agt	gca	agt	ata	gct	tta	gaa	aac	1117
Gln	Cys	Phe	Lys	Thr	Leu	Leu	Lys	Ser	Ala	Ser	Ile	Ala	Leu	Glu	Asn	
			340					345					350			
ttg	caa	aat	aac	cat	caa	atc	aca	gcc	gtt	aca	caa	gac	acg	caa	gaa	1165
Leu	Gln	Asn	Asn	His	Gln	Ile	Thr	Ala	Val	Thr	Gln	Asp	Thr	Gln	Glu	
		355				360						365				
aac	aca	aac	gcg	ctc	aaa	aat	act	act	caa	gat	ttt	aac	aaa	act	acc	1213
Asn	Thr	Asn	Ala	Leu	Lys	Asn	Thr	Thr	Gln	Asp	Phe	Asn	Lys	Thr	Thr	
	370					375					380					
aat	gaa	cca	aca	aac	cct	aac	aat	aac	tat	gga	atg	gat	ttt			1255
Asn	Glu	Pro	Thr	Asn	Pro	Asn	Asn	Asn	Tyr	Gly						

<213> Helicobacter pylori

<400> 112

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Lys	Ser	Phe	Arg	His	Glu	Asn	Tyr	Phe	Tyr	Lys	Val	Leu	Gly	Ser	Ala
			20					25					30		
Thr	Ser	Gln	Ile	Glu	Ser	Leu	Lys	Lys	Arg	Glu	Asn	Ala	Leu	Phe	Asp
		35					40					45			
His	Leu	Asp	Ser	Leu	Lys	Ser	Leu	Leu	Glu	Lys	Thr	His	Trp	Glu	Lys
	50					55					60				
Glu	Lys	Phe	Thr	Pro	Pro	Ile	Asn	Glu	Lys	Glu	Leu	Asn	Arg	Gln	Leu
65					70					75					80
Lys	Glu	Val	Arg	Trp	Phe	Asn	Lys	Glu	Thr	Pro	Thr	Ser	Lys	Asn	Thr
				85					90					95	
Tyr	Lys	Lys	Ile	Gln	Lys	Leu	Ala	Val	Tyr	Lys	Ser	Pro	Leu	Ile	Lys
			100					105					110		
Asp	Tyr	Leu	Tyr	Thr	Ile	Lys	Lys	Leu	Phe	Ala	Thr	Gln	Lys	Lys	Ile
		115					120					125			
Ile	Asp	Leu	Glu	Lys	Asn	Tyr	Lys	Asp	Leu	Arg	Ala	Leu	Lys	Glu	Glu
130						135						140			
Phe	Ser	Lys	Asp	Leu	Glu	Thr	Asp	Leu	Ser	His	Ser	Lys	Lys	Arg	Phe
145					150					155					160
Glu	Leu	Tyr	Thr	Arg	Leu	Lys	Ser	Met	Ser	Lys	Val	Phe	Ile	Ser	Lys
				165					170					175	
Ser	Ile	Val	Lys	Asn	Leu	Glu	Lys	Ile	Ala	Leu	Asp	Phe	Lys	Ser	Asp
			180					185					190		
Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn
	195						200					205			
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala
	210					215					220				
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu
225					230					235					240
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn
				245					250					255	
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg
			260					265					270		
Leu	Glu	Glu	Glu	Asn	Tyr	Cys	Phe	Ala	Lys	Lys	Arg	Lys	Glu	Phe	Leu
			275				280						285		
Glu	Thr	Arg	Ala	Met	Glu	Leu	Ser	Lys	Asp	Leu	Lys	Phe	Leu	Thr	Gln
	290					295					300				
Ala	Asn	Glu	Asn	Asp	Leu	Pro	Ile	Tyr	Glu	Arg	Gly	Gln	Arg	Asp	Lys
305					310					315					320
Ile	Ile	Lys	Arg	Cys	Glu	Lys	Ser	Leu	Asn	Phe	Leu	Gln	Lys	Glu	Leu
				325					330					335	
Gln	Cys	Phe	Lys	Thr	Leu	Leu	Lys	Ser	Ala	Ser	Ile	Ala	Leu	Glu	Asn
			340					345					350		
Leu	Gln	Asn	Asn	His	Gln	Ile	Thr	Ala	Val	Thr	Gln	Asp	Thr	Gln	Glu
		355					360					365			
Asn	Thr	Asn	Ala	Leu	Lys	Asn	Thr	Thr	Gln	Asp	Phe	Asn	Lys	Thr	Thr
	370					375					380				
Asn	Glu	Pro	Thr	Asn	Pro	Asn	Asn	Asn	Tyr	Gly	Met	Asp	Phe		
385					390					395					

<210> 113

<211> 630

<212> DNA

<213> Helicobacter pylori

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	12.3%
Divorced	8.2%
Widowed	1.0%
Education level	
High school or less	65.4%
College	34.6%
Income (USD/month)	
< 1000	25.3%
1000-2000	45.7%
> 2000	29.0%
Health insurance	
Medicaid	15.2%
Medicare	68.5%
Private	16.3%
Uninsured	0.0%
Comorbidities	
Hypertension	42.1%
Diabetes	18.7%
Cholesterol	35.4%
Smoking status	
Current	12.5%
Former	38.9%
Never	48.6%
Alcohol consumption	
Regular	10.1%
Occasional	22.3%
Never	67.6%

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<210> 114
<211> 138
<212> PRT
<213> Helicobacter pylori
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-125-

Asn	Lys	Glu	Val	Ile	Asp	Phe	Leu	Gly	Ser	Val	Phe	Ala	Lys	Val	Cys
	35						40					45			
Lys	Asp	Phe	Glu	Ser	Glu	Leu	Val	Glu	Phe	Asp	Gly	Glu	Ser	Asp	His
	50					55					60				
Val	His	Leu	Leu	Ile	Asn	Tyr	Pro	Pro	Lys	Val	Ser	Val	Ser	Lys	Leu
	65				70					75					80
Val	Asn	Ser	Leu	Lys	Gly	Val	Ser	Ser	Arg	Leu	Thr	Arg	Gln	His	His
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Phe	Lys	Ser	Val	Glu	Ala	Ser	Leu	Trp	Gly	Lys	His	Leu	Trp	Ser	Pro
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Ser	Tyr	Phe	Ala	Gly	Ser	Cys	Gly	Asp	Ala	Pro	Leu	Glu	Met	Ile	Lys
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 <213> Helicobacter pylori

<220>
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Ser Ser Ala Leu Ile Thr Pro Phe Lys Lys Asp Leu Ser Val Asp Glu						
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Ala Ala Tyr Glu Thr Leu Ile Lys Arg Gln Ile Phe Gln Gly Met Asp						
	25 30 35					
gca tgc gtg cct gtt ggc acg aca gga gaa tcc gcc acg ctc acc cac	259					
Ala Cys Val Pro Val Gly Thr Thr Gly Glu Ser Ala Thr Leu Thr His						
	40 45 50					
aaa gag cac atg cgt tgc att gaa atc gcc ata gaa act tgc aaa aac	307					
Lys Glu His Met Arg Cys Ile Glu Ile Ala Ile Glu Thr Cys Lys Asn						
	55 60 65					
act aaa acg ccc tca aat tcg cgc atg aaa gtg tta gcc ggc gtg ggc	355					
Thr Lys Thr Pro Ser Asn Ser Arg Met Lys Val Leu Ala Gly Val Gly						
	70 75 80 85					
agt aac gcc acg agc gag tcc ctt tct tta gca aag ttc gct caa aaa	403					
Ser Asn Ala Thr Ser Glu Ser Leu Ser Leu Ala Lys Phe Ala Gln Lys						
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Ile Gly Ala Asp Ala Ile Leu Cys Val Ser Pro Tyr Tyr Asn Arg Pro						
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Phe Gln Gly Met Asp Ala Cys Val Pro Val Gly Thr Thr Gly Glu Ser
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Leu Ala Gly Val Gly Ser Asn Ala Thr Ser Glu Ser Leu Ser Leu Ala
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Lys Phe Ala Gln Lys Ile Gly Ala Asp Ala Ile Leu Cys Val Ser Pro
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Tyr Tyr Asn Arg Pro Thr Gln Gln Gly Leu Phe Glu His Tyr Lys Thr
           115          120          125
Ile Ala Gln Ser Val Glu Ile Pro Val Met Leu Tyr Asp Val Pro Ser
           130          135          140
Arg Thr Gly Val Ser Ile Glu Val Pro Thr Ala Leu Lys Leu Phe Arg
           145          150          155          160
Glu Val Pro Asn Ile Lys Ala Ile Lys Glu Ala Ser Gly Ser Leu Lys
           165          170          175
Arg Val Thr Glu Leu His Tyr Tyr Glu Lys Asp Phe Lys Ile Phe Ser
           180          185          190
Gly Glu Asp Ser Leu Asn His Ser Ile Met Phe Ser Gly Gly Cys Gly
           195          200          205
Val Ile Ser Val Thr Gly Asn Leu Met Pro Asn Leu Ile Ser Gln Met
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Val Asn Cys Ala Leu Lys Gln Lys Tyr Gln Gln Ala Leu Glu Ile Gln
           225          230          235          240
Asn Lys Leu Phe Cys Leu His Gln Ala Leu Phe Val Glu Thr Asn Pro
           245          250          255
Ile Pro Ile Lys Met Ala Met His Leu Ala Gly Leu Ile Glu Asn Pro
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Ser Tyr Arg Leu Pro Leu Val Ala Pro Ser Lys Glu Thr Ile Gln Leu
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Leu Glu Lys Thr Leu Gln Gln Tyr Glu Val Ile Ala
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      Met Leu Leu Ile Val Phe Phe Lys Phe Tyr Phe Gln Tyr Ser
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att aaa aaa aaa tca ttt tat ttt att ttt gtt ata att caa gct att 157
Ile Lys Lys Lys Ser Phe Tyr Phe Ile Phe Val Ile Ile Gln Ala Ile
   15           20           25           30

ttt att ttc aat cta agg agg tgt cgc atg gac aat caa aag ata acg 205
Phe Ile Phe Asn Leu Arg Arg Cys Arg Met Asp Asn Gln Lys Ile Thr
           35           40           45

cat caa aat atc acg caa aaa caa ggc gag ctt aaa aga gac atg aaa 253

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Met	Arg	His	Leu	Leu	Met	Ile	Ala	Phe	Gly	Gly	Ala	Ile	Gly	Thr	Gly	
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ctt	ttt	gta	ggc	act	ggg	ggg	aat	att	gcg	agc	gct	ggc	cct	tta	ggg	349
Leu	Phe	Val	Gly	Thr	Gly	Gly	Asn	Ile	Ala	Ser	Ala	Gly	Pro	Leu	Gly	
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Thr	Leu	Ile	Ala	Tyr	Cys	Phe	Gly	Gly	Leu	Val	Val	Tyr	Cys	Ile	Met	
	95				100					105					110	
ctc	tct	tta	ggc	gaa	ttg	gct	agc	gtt	tat	ccc	act	aca	gga	agt	ttt	445
Leu	Ser	Leu	Gly	Glu	Leu	Ala	Ser	Val	Tyr	Pro	Thr	Thr	Gly	Ser	Phe	
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Gly	Asp	Tyr	Ala	Ala	Lys	Phe	Ile	Gly	Pro	Gly	Thr	Gly	Tyr	Met	Val	
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Phe	Trp	Met	Tyr	Trp	Leu	Gly	Trp	Val	Ile	Thr	Val	Ala	Leu	Glu	Tyr	
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Ile	Ala	Ile	Gly	Met	Leu	Met	Gln	Arg	Trp	Phe	Ala	Asp	Ile	Pro	Ile	
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His	Tyr	Trp	Val	Ile	Leu	Cys	Ile	Ala	Leu	Val	Phe	Leu	Leu	Asn	Phe	
	175				180					185					190	
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Phe	Ser	Val	Lys	Ile	Phe	Ala	Glu	Gly	Glu	Phe	Phe	Phe	Ser	Leu	Ile	
				195				200					205			
aaa	gtt	tta	gcg	gtg	atc	gct	ttt	ata	ggc	att	ggc	gcg	att	ggg	att	733
Lys	Val	Leu	Ala	Val	Ile	Ala	Phe	Ile	Gly	Ile	Gly	Ala	Ile	Gly	Ile	
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Ile	Tyr	Gln	Ile	Tyr	Ser	His	Gly	Phe	Gly	Ser	Ile	Phe	Asp	Asn	Phe	
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His	Phe	Gly	Asp	Lys	Gly	Phe	Phe	Pro	Asn	Gly	Ser	Ala	Ala	Val	Phe	
	240					245					250					
agc	gcg	atg	ctc	gct	gtt	att	ttt	gct	ttc	act	ggc	aca	gag	gtg	att	877
Ser	Ala	Met	Leu	Ala	Val	Ile	Phe	Ala	Phe	Thr	Gly	Thr	Glu	Val	Ile	
	255				260					265					270	
ggg	gtg	gct	gtg	gga	gag	act	aaa	aac	gct	agc	gaa	gtg	atg	ccc	aaa	925
Gly	Val	Ala	Val	Gly	Glu	Thr	Lys	Asn	Ala	Ser	Glu	Val	Met	Pro	Lys	
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<213> Helicobacter pylori

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Phe Asn Leu Arg Arg Cys Arg Met Asp Asn Gln Lys Ile Thr His Gln
35 40 45
Asn Ile Thr Gln Lys Gln Gly Glu Leu Lys Arg Asp Met Lys Met Arg
50 55 60
His Leu Leu Met Ile Ala Phe Gly Gly Ala Ile Gly Thr Gly Leu Phe
65 70 75 80
Val Gly Thr Gly Gly Asn Ile Ala Ser Ala Gly Pro Leu Gly Thr Leu
85 90 95
Ile Ala Tyr Cys Phe Gly Gly Leu Val Val Tyr Cys Ile Met Leu Ser
100 105 110
Leu Gly Glu Leu Ala Ser Val Tyr Pro Thr Thr Gly Ser Phe Gly Asp
115 120 125
Tyr Ala Ala Lys Phe Ile Gly Pro Gly Thr Gly Tyr Met Val Phe Trp
130 135 140
Met Tyr Trp Leu Gly Trp Val Ile Thr Val Ala Leu Glu Tyr Ile Ala
145 150 155 160
Ile Gly Met Leu Met Gln Arg Trp Phe Ala Asp Ile Pro Ile His Tyr
165 170 175
Trp Val Ile Leu Cys Ile Ala Leu Val Phe Leu Leu Asn Phe Phe Ser
180 185 190
Val Lys Ile Phe Ala Glu Gly Glu Phe Phe Phe Ser Leu Ile Lys Val
195 200 205
Leu Ala Val Ile Ala Phe Ile Gly Ile Gly Ala Ile Gly Ile Ile Tyr
210 215 220
Gln Ile Tyr Ser His Gly Phe Gly Ser Ile Phe Asp Asn Phe His Phe
225 230 235 240
Gly Asp Lys Gly Phe Phe Pro Asn Gly Ser Ala Ala Val Phe Ser Ala
245 250 255
Met Leu Ala Val Ile Phe Ala Phe Thr Gly Thr Glu Val Ile Gly Val
260 265 270
Ala Val Gly Glu Thr Lys Asn Ala Ser Glu Val Met Pro Lys Ala Ile
275 280 285
Lys Ala Thr Leu Trp Arg Ile Val Phe Phe Phe Leu Gly Ser Val Phe
290 295 300
Val Ile Ser Val Phe Leu Pro Met Asn Asp Ser Ser Ile Thr Gln Ser
305 310 315 320
Pro Phe Val Ser Val Leu Glu Arg Ile Asn Leu Pro Phe Ile Gly Met
325 330 335
Gly Ile Pro Tyr Val Ala Asp Ile Met Asn Ala Val Ile Ile Thr Ala
340 345 350
Met Phe Ser Thr Ala Asn Ser Gly Leu Tyr Gly Ala Ser Arg Met Ile
355 360 365
Tyr Gly Leu Ser Lys Gln Lys Met Phe Phe Lys Val Phe Ser Gln Leu
370 375 380
Asn Arg Gln Gly Thr Pro Thr Tyr Ala Met Phe Phe Ser Leu Ser Phe

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aat Asn	tcc Ser	ggc Gly	ggc Gly 135	gct Ala	tta Leu	att Ile	gat Asp	agc Ser 140	cgt Arg	gga Gly	ggg Gly	tta Leu	gtg Val 145	ggg Gly	att Ile	670
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tta Leu 260	aaa Lys	gtc Val	att Ile	aga Arg	gac Asp 265	aaa Lys	aaa Lys	gaa Glu	cgc Arg	gct Ala 270	ttc Phe	acc Thr	ctc Leu	act Thr	cta Leu 275	1054
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gaa Glu	acc Thr 310	aaa Lys	agg Arg	tct Ser	atg Met	cgt Arg	ttg Leu 315	agc Ser	gat Asp	gat Asp	gtt Val 320	caa Gln	ggg Gly	gtt Val	tta Leu	1198
gtc Val 325	tct Ser	caa Gln	gtg Val	aat Asn	gaa Glu	aat Asn 330	tcc Ser	cca Pro	gca Ala	gag Glu 335	caa Gln	gcc Ala	gga Gly	ttt Phe	agg Arg	1246

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Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val Lys Ser Val	
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Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg	
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Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys	
375 380 385	
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<211> 387

<212> PRT

<213> Helicobacter pylori

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Ala Thr Leu Val Gly Thr Asp Ser Glu Ser Asp Leu Ala Val Ile Arg	
50 55 60	
Ile Thr Lys Asp Asn Leu Pro Thr Ile Lys Phe Ser Asp Ser Asn Asp	
65 70 75 80	
Ile Ser Val Gly Asp Leu Val Phe Ala Ile Gly Asn Pro Phe Gly Val	
85 90 95	
Gly Glu Ser Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly	
100 105 110	
Ile Gly Ile Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile	
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Asn Pro Gly Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu	
130 135 140	
Val Gly Ile Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly	
145 150 155 160	
Ile Gly Phe Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln	
165 170 175	
Leu Ile Lys Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu	
180 185 190	
Gln Asp Leu Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly	
195 200 205	
Ala Val Val Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly	
210 215 220	
Ile Leu Val Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys	
225 230 235 240	
Asn Thr Asn Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln	
245 250 255	
Arg Val Thr Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr	
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[illegible]

<400> 121

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Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile Asn Ala Ala Tyr Glu Ile
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Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr Asp Gln Phe Gly Asp Asn
55 60 65 70

Met Phe Gly Gly Gln Asn Phe Ser Asp Phe Ala Arg Ser Arg Gly Pro
75 80 85

Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser Ile Phe Gly Lys Gly Gly
90 95 100

Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln Gly Phe Ser Gly Phe Asn
105 110 115

Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp Ile Thr Ala Ala Leu Asn

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Asn	Asn	Glu	Thr	Phe	Ser	Leu	Lys	Ile	Pro	Ile	Gly	Val	Glu	Glu	Gly					
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Glu	Lys	Ile	Arg	Val	Arg	Asn	Lys	Gly	Lys	Thr	Gly	Arg	Thr	Thr	Arg					
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Gly	Asp	Leu	Leu	Leu	Glu	Ile	His	Ile	Glu	Glu	Asp	Glu	Met	Tyr	Arg					
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Thr	Leu	Thr	Ile	Pro	Pro	Asn	Thr	Lys	Ala	Met	Gln	Lys	Phe	Arg	Ile					
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aaa	gaa	aaa	ggg	atc	aaa	aac	aga	aaa	act	tcg	cat	gtg	ggg	gat	ttg	824				
Lys	Glu	Lys	Gly	Ile	Lys	Asn	Arg	Lys	Thr	Ser	His	Val	Gly	Asp	Leu					
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Tyr	Leu	Gln	Ala	Arg	Leu	Ile	Leu	Pro	Lys	Thr	Glu	Thr	Leu	Ser	Asn					
265					270					275										
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Glu	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Glu	Leu											
280					285															
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			20					25					30		
Pro	Asp	Leu	Asn	Lys	Thr	Lys	Glu	Ala	Glu	Glu	Lys	Phe	Lys	Glu	Ile
		35					40					45			
Asn	Ala	Ala	Tyr	Glu	Ile	Leu	Ser	Asp	Glu	Glu	Lys	Arg	Arg	Gln	Tyr
	50					55					60				

Asp Gln Phe Gly Asp Asn Met Phe Gly Gly Gln Asn Phe Ser Asp Phe
65 70 75 80
Ala Arg Ser Arg Gly Pro Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser
85 90 95
Ile Phe Gly Lys Gly Gly Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln
100 105 110
Gly Phe Ser Gly Phe Asn Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp
115 120 125
Ile Thr Ala Ala Leu Asn Val Ser Val Leu Asp Thr Leu Leu Gly Asn
130 135 140
Lys Lys Gln Val Ser Ile Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro
145 150 155 160
Ile Gly Val Glu Glu Gly Glu Lys Ile Arg Val Arg Asn Lys Gly Lys
165 170 175
Thr Gly Arg Thr Thr Arg Gly Asp Leu Leu Leu Glu Ile His Ile Glu
180 185 190
Glu Asp Glu Met Tyr Arg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe
195 200 205
Asp Leu Pro Leu Lys Thr Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala
210 215 220
Thr Trp His Lys Thr Leu Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala
225 230 235 240
Met Gln Lys Phe Arg Ile Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr
245 250 255
Ser His Val Gly Asp Leu Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys
260 265 270
Thr Glu Thr Leu Ser Asn Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu
275 280 285

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<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (113)...(1285)

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Met Ser
1

ctg act tcg ctt tta aac cca aaa agc cta gaa gat ttt tta ggc caa 166
Leu Thr Ser Leu Leu Asn Pro Lys Ser Leu Glu Asp Phe Leu Gly Gln
5 10 15

gag cat tta gta ggg aaa gac gcc ccc tta ttt aaa gcc cta caa tcc 214
Glu His Leu Val Gly Lys Asp Ala Pro Leu Phe Lys Ala Leu Gln Ser
20 25 30

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Lys His Phe Pro His Ala Phe Phe Tyr Gly Pro Pro Gly Val Gly Lys
35 40 45 50

aca agc ctg gct caa atc atc gcc tat atg cta gag cgc ccc att ctt 310
Thr Ser Leu Ala Gln Ile Ile Ala Tyr Met Leu Glu Arg Pro Ile Leu
55 60 65

tta	ttc	aat	gcg	acg	gat	ttt	aaa	tta	gag	gat	ttg	cgc	ctt	aag	ctt	358
Leu	Phe	Asn	Ala	Thr	Asp	Phe	Lys	Leu	Glu	Asp	Leu	Arg	Leu	Lys	Leu	
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Lys	Asn	Tyr	Gln	Asn	Thr	Leu	Leu	Lys	Pro	Val	Val	Phe	Ile	Asp	Glu	
			85				90			95						
acc	cac	aga	ttg	aat	aaa	acc	caa	caa	gaa	ttt	tta	ctc	ccc	att	atg	454
Thr	His	Arg	Leu	Asn	Lys	Thr	Gln	Gln	Glu	Phe	Leu	Leu	Pro	Ile	Met	
			100				105			110						
gaa	aaa	gat	cac	gct	tta	att	tta	ggg	gct	agc	acg	caa	gat	cct	aat	502
Glu	Lys	Asp	His	Ala	Leu	Ile	Leu	Gly	Ala	Ser	Thr	Gln	Asp	Pro	Asn	
			115				120			125			130			
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Tyr	Ser	Leu	Ser	His	Ala	Ile	Arg	Ser	Arg	Ser	Phe	Ile	Phe	Glu	Leu	
			135				140			145						
acc	ccc	cta	aac	aag	agc	gat	tta	gac	agg	ctt	tgc	gct	aaa	gct	tta	598
Thr	Pro	Leu	Asn	Lys	Ser	Asp	Leu	Asp	Arg	Leu	Cys	Ala	Lys	Ala	Leu	
			150				155			160						
aca	ttg	ctc	aaa	aaa	caa	ata	gag	cct	ggc	gct	aaa	acc	tat	ctt	tta	646
Thr	Leu	Leu	Lys	Lys	Gln	Ile	Glu	Pro	Gly	Ala	Lys	Thr	Tyr	Leu	Leu	
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Asn	Asn	Ser	Ala	Gly	Asp	Ala	Arg	Ala	Leu	Leu	Asn	Leu	Leu	Asp	Leu	
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agc	gct	aaa	ata	gaa	gat	cct	atc	act	tta	aaa	acg	cta	caa	tcc	tta	742
Ser	Ala	Lys	Ile	Glu	Asp	Pro	Ile	Thr	Leu	Lys	Thr	Leu	Gln	Ser	Leu	
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Arg	Pro	His	Ser	Leu	Asn	Asp	Gly	Ser	Tyr	Ser	Asp	Asp	Thr	His	Tyr	
			215				220			225						
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Asn	Leu	Thr	Ser	Ala	Leu	Ile	Lys	Ser	Leu	Arg	Gly	Ser	Asp	Glu	Asn	
			230				235			240						
gct	tcc	atc	tat	tat	ctg	gcg	cgc	ttg	att	gct	ggc	ggg	gaa	aac	ccg	886
Ala	Ser	Ile	Tyr	Tyr	Leu	Ala	Arg	Leu	Ile	Ala	Gly	Gly	Glu	Asn	Pro	
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Glu	Phe	Ile	Ala	Arg	Arg	Leu	Val	Ile	Phe	Ala	Ser	Glu	Asp	Ile	Gly	
			260				265			270						
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Asn	Ala	Asn	Pro	Asn	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Cys	Leu	Phe	Ala	
			275				280			285			290			
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Val	Lys	Gln	Ile	Gly	Tyr	Pro	Glu	Ala								

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Ile	Asn	Gln	Ala	Leu	Asp	Cys	Val	Gln	Lys	Gly	Ser	Leu	Tyr	Pro	Ile															
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Tyr	Asn	Gly	Tyr	Val	Lys	Gln	Asp	Tyr	Leu	Glu	Lys	Pro	Leu	Asp	Leu															
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Gln	Ser	Lys	His	Phe	Pro	His	Ala	Phe	Phe	Tyr	Gly	Pro	Pro	Gly	Val															
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Gly	Lys	Thr	Ser	Leu	Ala	Gln	Ile	Ile	Ala	Tyr	Met	Leu	Glu	Arg	Pro															
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Lys	Leu	Lys	Asn	Tyr	Gln	Asn	Thr	Leu	Leu	Lys	Pro	Val	Val	Phe	Ile															
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145				150				155				160																		
Ala	Leu	Thr	Leu	Leu	Lys	Lys	Gln	Ile	Glu	Pro	Gly	Ala	Lys	Thr	Tyr															
165				170				175																						
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Ser	Leu	Arg	Pro	His	Ser	Leu	Asn	Asp	Gly	Ser	Tyr	Ser	Asp	Asp	Thr
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His	Tyr	Asn	Leu	Thr	Ser	Ala	Leu	Ile	Lys	Ser	Leu	Arg	Gly	Ser	Asp
225					230					235					240
Glu	Asn	Ala	Ser	Ile	Tyr	Tyr	Leu	Ala	Arg	Leu	Ile	Ala	Gly	Gly	Glu
				245					250					255	
Asn	Pro	Glu	Phe	Ile	Ala	Arg	Arg	Leu	Val	Ile	Phe	Ala	Ser	Glu	Asp
			260					265					270		
Ile	Gly	Asn	Ala	Asn	Pro	Asn	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Cys	Leu
		275					280						285		
Phe	Ala	Val	Lys	Gln	Ile	Gly	Tyr	Pro	Glu	Ala	Arg	Ile	Ile	Leu	Ser
290					295						300				
Gln	Cys	Val	Ile	Tyr	Leu	Ala	Cys	Ser	Pro	Lys	Ser	Asn	Thr	Ala	Tyr
305					310					315					320
Arg	Ala	Ile	Asn	Gln	Ala	Leu	Asp	Cys	Val	Gln	Lys	Gly	Ser	Leu	Tyr
				325					330					335	
Pro	Ile	Pro	Lys	His	Leu	Leu	Pro	Asn	Ala	Lys	Asp	Tyr	Leu	Tyr	Pro
			340					345					350		
His	Asp	Tyr	Asn	Gly	Tyr	Val	Lys	Gln	Asp	Tyr	Leu	Glu	Lys	Pro	Leu
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Asp	Leu	Val	Ser	Ser	Gln	Gly	Ile	Gly	Phe	Glu	Lys	Thr	Leu	Leu	Glu
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		Met Gly Phe Tyr	Ala Gly Leu	Asn Ala Leu	Asp Tyr										
		1		5											
gac acc ata gac cca aaa tac tac aag tat atc aag tat tat aaa gcc															159
Asp Thr Ile	Asp Pro Lys Tyr	Tyr Tyr Lys Tyr	Ile Lys Tyr Tyr	Lys Ala											
	15		20		25										
tat gag gat aaa gaa gtt gaa gaa ttg atc aga gac tta aaa agg gcg															207
Tyr Glu Asp	Lys Glu Val	Glu Glu Leu	Ile Arg Asp	Leu Lys Arg	Ala										
	30		35		40										
aac gct aaa agc ggg ctt att tta ggg atc aat acc ggg ttt ttt tac															255
Asn Ala Lys	Ser Gly Leu	Ile Leu Gly	Ile Asn Thr	Gly Phe Phe	Tyr										
	45		50		55										60
aat cat gaa atc atg gtt aga act aat agc tct agc atc acg ggg aat															303
Asn His Glu	Ile Met Val	Arg Thr Asn	Ser Ser Ser	Ile Thr Gly	Asn										
	65		70		75										
att tta aat tat ttg ttc gct tac ggc ttg cgt ttt ggc tat caa act															351
Ile Leu Asn	Tyr Leu Phe	Ala Tyr Gly	Leu Arg Phe	Gly Tyr Gln	Thr										

80	85	90	
ttc agg ccg tcg ttt ttt gcg cgc ttg gtc aag cca aat atc att ggc Phe Arg Pro Ser Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly 95 100 105			399
agg cgc att tat atc caa tat tat gga gga gct cct aaa aaa gcg ggc Arg Arg Ile Tyr Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly 110 115 120			447
ttt ggg gat gta ggg ttt caa tcg gtt atg ctg aat ggg gat ttt tta Phe Gly Asp Val Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu 125 130 135 140			495
ttg gat ttt cct ttg cct ttt gtg ggg aaa tac ctt tat atg ggg ggt Leu Asp Phe Pro Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly 145 150 155			543
tat atg ggt tta ggt ttg ggg gtt gta gcg cat ggg gtg aat tac acg Tyr Met Gly Leu Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr 160 165 170			591
gcg gaa tgg ggg atg tct ttt aac gca gga ttg gct cta acg gta tta Ala Glu Trp Gly Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu 175 180 185			639
gaa aaa aac cgc att gaa ttt gga ttt aaa att ttg aat aat ttc cct Glu Lys Asn Arg Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro 190 195 200			687
ttt ttg caa tct aat tct tca aaa gag act tgg tgg gga gct atg gca Phe Leu Gln Ser Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala 205 210 215 220			735
aac att ggg tat caa tat gtg ttc taaaaaaaaata agaaatctca ttttatgctt Asn Ile Gly Tyr Gln Tyr Val Phe 225			789
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Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala Tyr Glu Asp Lys 20 25 30	
Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala Asn Ala Lys Ser 35 40 45	
Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr Asn His Glu Ile 50 55 60	
Met Val Arg Thr Asn Ser Ser Ser Ile Thr Gly Asn Ile Leu Asn Tyr 65 70 75 80	
Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr Phe Arg Pro Ser 85 90 95	

Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly Arg Arg Ile Tyr
 100 105 110
 Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly Phe Gly Asp Val
 115 120 125
 Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu Leu Asp Phe Pro
 130 135 140
 Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly Tyr Met Gly Leu
 145 150 155 160
 Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr Ala Glu Trp Gly
 165 170 175
 Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu Glu Lys Asn Arg
 180 185 190
 Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro Phe Leu Gln Ser
 195 200 205
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 210 215 220
 Gln Tyr Val Phe
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 Met Lys Glu Arg Ile Val Asn Leu
 1 5
 gaa act ttg gat ttt gaa att tct caa gaa gtg agt ttg cgc cct agt 160
 Glu Thr Leu Asp Phe Glu Ile Ser Gln Glu Val Ser Leu Arg Pro Ser
 10 15 20
 ctt tgg gaa gat ttt atc ggt caa gaa aag att aaa agc aat ttg caa 208
 Leu Trp Glu Asp Phe Ile Gly Gln Glu Lys Ile Lys Ser Asn Leu Gln
 25 30 35 40
 att tct att tgc gcg gct aaa aaa cgc caa gaa agt ttg gat cac atg 256
 Ile Ser Ile Cys Ala Ala Lys Lys Arg Gln Glu Ser Leu Asp His Met
 45 50 55
 ctt ttt ttt ggc ccg ccc ggt ttg ggt aaa act tca atc agc cat atc 304
 Leu Phe Phe Gly Pro Pro Gly Leu Gly Lys Thr Ser Ile Ser His Ile
 60 65 70
 atc gct aaa gaa atg gaa acc aat atc aag atc acc gcc gct ccc atg 352
 Ile Ala Lys Glu Met Glu Thr Asn Ile Lys Ile Thr Ala Ala Pro Met
 75 80 85
 ata gaa aaa agc ggt gat tta gcc gcc att ttg acc aat ttg caa gct 400
 Ile Glu Lys Ser Gly Asp Leu Ala Ala Ile Leu Thr Asn Leu Gln Ala
 90 95 100
 aaa gac att ctt ttt att gat gaa atc cac cgg ctc agc cca gcg att 448

Lys	Asp	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Arg	Leu	Ser	Pro	Ala	Ile		
105					110					115					120		
gaa	gag	gtt	tta	tac	ccg	gcg	atg	gaa	gat	ttt	agg	ttg	gat	att	atc		496
Glu	Glu	Val	Leu	Tyr	Pro	Ala	Met	Glu	Asp	Phe	Arg	Leu	Asp	Ile	Ile		
				125					130					135			
ata	ggc	tca	ggc	cca	gcg	gct	caa	acc	att	aaa	att	gat	tta	ccc	cct		544
Ile	Gly	Ser	Gly	Pro	Ala	Ala	Gln	Thr	Ile	Lys	Ile	Asp	Leu	Pro	Pro		
			140					145					150				
ttc	act	ctc	atc	ggc	gct	acc	acc	aga	gcc	gga	atg	ctc	tct	aac	ccc		592
Phe	Thr	Leu	Ile	Gly	Ala	Thr	Thr	Arg	Ala	Gly	Met	Leu	Ser	Asn	Pro		
		155					160					165					
tta	aga	gac	aga	ttt	ggc	atg	agt	ttt	aga	atg	caa	ttt	tat	aac	cct		640
Leu	Arg	Asp	Arg	Phe	Gly	Met	Ser	Phe	Arg	Met	Gln	Phe	Tyr	Asn	Pro		
	170					175					180						
agc	gaa	ctg	gcc	ctc	atc	att	aaa	aaa	gct	gcc	gtt	aaa	ctc	aac	caa		688
Ser	Glu	Leu	Ala	Leu	Ile	Ile	Lys	Lys	Ala	Ala	Val	Lys	Leu	Asn	Gln		
185					190					195					200		
gac	atc	aaa	caa	gaa	agt	gct	gat	gaa	atc	gct	aaa	agg	agt	aga	ggc		736
Asp	Ile	Lys	Gln	Glu	Ser	Ala	Asp	Glu	Ile	Ala	Lys	Arg	Ser	Arg	Gly		
			205						210					215			
acg	cca	agg	atc	gct	tta	agg	ctt	tta	aaa	agg	gtg	cgc	gat	ttt	gcg		784
Thr	Pro	Arg	Ile	Ala	Leu	Arg	Leu	Leu	Lys	Arg	Val	Arg	Asp	Phe	Ala		
			220				225						230				
cta	gtc	aaa	aat	tca	agc	ttg	atg	gat	tta	aac	atc	act	ttg	cat	gct		832
Leu	Val	Lys	Asn	Ser	Ser	Leu	Met	Asp	Leu	Asn	Ile	Thr	Leu	His	Ala		
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Leu	Asn	Glu	Leu	Gly	Val	Asn	Glu	Leu	Gly	Phe	Asp	Glu	Ala	Asp	Leu		
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gcg	tat	tta	tct	ttg	ttg	gct	aac	gct	caa	gga	aag	ccg	gtg	ggt	ttg		928
Ala	Tyr	Leu	Ser	Leu	Leu	Ala	Asn	Ala	Gln	Gly	Lys	Pro	Val	Gly	Leu		
265					270					275					280		
aac	acg	att	gca	gca	tct	atg	aga	gaa	gat	gaa	ggc	acg	att	gaa	gac		976
Asn	Thr	Ile	Ala	Ala	Ser	Met	Arg	Glu	Asp	Glu	Gly	Thr	Ile	Glu	Asp		
				285					290					295			
gtg	att	gag	cct	ttt	tta	ctc	gct	aat	ggg	tat	tta	gag	cgc	acc	gct		1024
Val	Ile	Glu	Pro	Phe	Leu	Leu	Ala	Asn	Gly	Tyr	Leu	Glu	Arg	Thr	Ala		
			300					305					310				
aaa	ggc	aga	atc	gcc	acg	cct	aaa	acc	cat	gag	ctc	tta	aaa	atc	ccc		1072
Lys	Gly	Arg	Ile	Ala	Thr	Pro	Lys	Thr	His	Glu	Leu	Leu	Lys	Ile	Pro		
		315					320					325					
act	tta	aac	ccc	caa	act	tta	ttt	taat	ctt	ggt	tagaa	agaaa	attac	actac			1126
Thr	Leu	Asn	Pro	Gln	Thr	Leu	Phe										
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1171

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 <212> PRT
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 Glu Lys Ile Lys Ser Asn Leu Gln Ile Ser Ile Cys Ala Ala Lys Lys
 35 40 45
 Arg Gln Glu Ser Leu Asp His Met Leu Phe Phe Gly Pro Pro Gly Leu
 50 55 60
 Gly Lys Thr Ser Ile Ser His Ile Ile Ala Lys Glu Met Glu Thr Asn
 65 70 75 80
 Ile Lys Ile Thr Ala Pro Met Ile Glu Lys Ser Gly Asp Leu Ala
 85 90 95
 Ala Ile Leu Thr Asn Leu Gln Ala Lys Asp Ile Leu Phe Ile Asp Glu
 100 105 110
 Ile His Arg Leu Ser Pro Ala Ile Glu Glu Val Leu Tyr Pro Ala Met
 115 120 125
 Glu Asp Phe Arg Leu Asp Ile Ile Ile Gly Ser Gly Pro Ala Ala Gln
 130 135 140
 Thr Ile Lys Ile Asp Leu Pro Pro Phe Thr Leu Ile Gly Ala Thr Thr
 145 150 155 160
 Arg Ala Gly Met Leu Ser Asn Pro Leu Arg Asp Arg Phe Gly Met Ser
 165 170 175
 Phe Arg Met Gln Phe Tyr Asn Pro Ser Glu Leu Ala Leu Ile Ile Lys
 180 185 190
 Lys Ala Ala Val Lys Leu Asn Gln Asp Ile Lys Gln Glu Ser Ala Asp
 195 200 205
 Glu Ile Ala Lys Arg Ser Arg Gly Thr Pro Arg Ile Ala Leu Arg Leu
 210 215 220
 Leu Lys Arg Val Arg Asp Phe Ala Leu Val Lys Asn Ser Ser Leu Met
 225 230 235 240
 Asp Leu Asn Ile Thr Leu His Ala Leu Asn Glu Leu Gly Val Asn Glu
 245 250 255
 Leu Gly Phe Asp Glu Ala Asp Leu Ala Tyr Leu Ser Leu Leu Ala Asn
 260 265 270
 Ala Gln Gly Lys Pro Val Gly Leu Asn Thr Ile Ala Ala Ser Met Arg
 275 280 285
 Glu Asp Glu Gly Thr Ile Glu Asp Val Ile Glu Pro Phe Leu Leu Ala
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                                   Met Phe
                                   1

gaa gat tta aaa ccg cat tta cag gaa tta aga aag cgt ttg atg gtt      164
Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu Met Val
                                   5                                10                                15

tct gta gga acg att cta gtg gcg ttt ttg ggg tgc ttt cat ttt tgg      212
Ser Val Gly Thr Ile Leu Val Ala Phe Leu Gly Cys Phe His Phe Trp
                                   20                                25                                30

aaa agt att ttt gaa ttt gtt aaa aat tcc tat aaa ggc acg ctc att      260
Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr Leu Ile
                                   35                                40                                45                                50

cag ctc tcc cct att gaa ggg gtc atg gta gcg gtt aaa atc agt ttt      308
Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile Ser Phe
                                   55                                60                                65

tca gcc gct atc gtc att tcc atg ccc att att ttt tgg caa tta tgg      356
Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln Leu Trp
                                   70                                75                                80

ctc ttt atc gct cca ggg ctt tac aag aat gaa aaa aaa gtg att ttg      404
Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val Ile Leu
                                   85                                90                                95

cct ttt gtg ttt ttt ggg agt ggg atg ttt ttg att ggg gcg gcg ttt      452
Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala Ala Phe
                                   100                               105                               110

tct tat tat gtg gtg ttc cct ttc att att gaa tac tta gcc act ttt      500
Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala Thr Phe
                                   115                               120                               125                               130

ggg agc gat gtg ttt gcg gct aat att tct gcg tcc agt tac gtg agc      548
Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr Val Ser
                                   135                               140                               145

ttt ttc acg cgc ttg att tta ggc ttt ggc gtg gcg ttt gaa ttg cct      596
Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu Leu Pro
                                   150                               155                               160

gtt ttg gcg tat ttt ttg gct aaa gtg ggc ttg att act gat gcg agc      644
Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp Ala Ser
                                   165                               170                               175

ttg aaa gcg tat ttt aaa tac gct att gta gtg att ttt att gta gca      692
Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile Val Ala
                                   180                               185                               190

gcc att atc act ccc cct gat gtg gtg agt caa atc ttt atg gcg ttg      740
Ala Ile Ile Thr Pro Pro Asp Val Val Ser Gln Ile Phe Met Ala Leu
                                   195                               200                               205                               210

ccc tta gtg ggg ctt tat ggg ctt tct att tta atc gcc aaa atg gtc      788

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Pro Leu Val Gly Leu Tyr Gly Leu Ser Ile Leu Ile Ala Lys Met Val
215 220 225

aat ccg gct ccc aaa gat aac gaa aat aac aac gaa aat aat aac gaa 836
Asn Pro Ala Pro Lys Asp Asn Glu Asn Asn Asn Glu Asn Asn Asn Glu
230 235 240

aat aac acc aaa gag aat aca aag agc gag tcg tagttgaaag aatttgattt 889
Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser
245 250

agaaagctat gattattatt tgcctaagga attgatcgca agctaccccg ttttgcccaa 949
agaaaaggct aaattactcg tctatgaaag gcgttcgcaa 989

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<212> PRT
<213> Helicobacter pylori

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20 25 30

Phe Trp Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr
35 40 45

Leu Ile Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile
50 55 60

Ser Phe Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln
65 70 75 80

Leu Trp Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val
85 90 95

Ile Leu Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala
100 105 110

Ala Phe Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala
115 120 125

Thr Phe Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr
130 135 140

Val Ser Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu
145 150 155 160

Leu Pro Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp
165 170 175

Ala Ser Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile
180 185 190

Val Ala Ala Ile Ile Thr Pro Pro Asp Val Val Ser Gln Ile Phe Met
195 200 205

Ala Leu Pro Leu Val Gly Leu Tyr Gly Leu Ser Ile Leu Ile Ala Lys
210 215 220

Met Val Asn Pro Ala Pro Lys Asp Asn Glu Asn Asn Asn Glu Asn Asn
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Asn Glu Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser
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Ala Glu Asn Leu Ser Tyr Met Ser Ser Ser Tyr Gln Ile Gly Thr Val
10 15 20

ttt atg cgc cct tta aac acc aac aag ctt tta caa ggg gct tca atc 150
Phe Met Arg Pro Leu Asn Thr Asn Lys Leu Leu Gln Gly Ala Ser Ile
25 30 35 40

cct caa ggc tat gaa gtg aat cct aaa aac gat tgg gct tat tct agg 198
Leu Gln Gly Tyr Glu Val Asn Pro Lys Asn Asp Trp Ala Tyr Ser Arg
 45 50 55

tat tat ttc ttt ata gat tat ggc aat gtg ctt ttt aat aat gac tct 246
Tyr Tyr Phe Phe Ile Asp Tyr Gly Asn Val Leu Phe Asn Asn Asp Ser
60 65 70

act tta caa gcg aac atg ttc act tat ggg gtg gga ggg gat ttt atg 294
Thr Leu Gln Ala Asn Met Phe Thr Tyr Gly Val Gly Gly Asp Phe Met
75 80 85

gtc gcc tac gct aaa aac cct atc aac cgc tgg gct ttt ttc ttt ggc 342
Val Ala Tyr Ala Lys Asn Pro Ile Asn Arg Trp Ala Phe Phe Phe Gly
90 95 100

ttg	caa	ctg	gcc	gct	aac	aca	tgg	ata	ctc	aac	aat	aaa	gtc	aaa	gat	390
Leu	Gln	Leu	Ala	Ala	Asn	Thr	Trp	Ile	Leu	Asn	Asn	Lys	Val	Lys	Asp	
105					110					115					120	

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Leu Val Val Asn Thr Trp Asp Ser Leu Lys Asp Phe Asn Phe His Asn
125 130 135

act tat ttc agg gct att ggg aag ttt ggg gtg cag ttt cgc acg atc 486
Thr Tyr Phe Arg Ala Ile Gly Lys Phe Gly Val Gln Phe Arg Thr Ile
140 145 150

ggt ttg tat cat aag gtg gat gta gaa att ggc atg aaa atc ttt cta 534
Val Leu Tyr His Lys Val Asp Val Glu Ile Gly Met Lys Ile Phe Leu
155 160 165

act cct gaa agg cgc agt ttg ttt gaa agg agc ttt ttg ttt ttt gtt 582
Thr Pro Glu Arg Arg Ser Leu Phe Glu Arg Ser Phe Leu Phe Phe Val
170 175 180

tgc cat tgc tgg cat ttt taaatggcgg agagagaggg attcgaaccc 630
Ser His Ser Trp His Phe
185 190

tcgaaggctt gcaccttaca cgcgt 655

-147-

<211> 190
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 Lys Leu Leu Gln Gly Ala Ser Ile Leu Gln Gly Tyr Glu Val Asn Pro
 35 40 45
 Lys Asn Asp Trp Ala Tyr Ser Arg Tyr Tyr Phe Phe Ile Asp Tyr Gly
 50 55 60
 Asn Val Leu Phe Asn Asn Asp Ser Thr Leu Gln Ala Asn Met Phe Thr
 65 70 75 80
 Tyr Gly Val Gly Gly Asp Phe Met Val Ala Tyr Ala Lys Asn Pro Ile
 85 90 95
 Asn Arg Trp Ala Phe Phe Phe Gly Leu Gln Leu Ala Ala Asn Thr Trp
 100 105 110
 Ile Leu Asn Asn Lys Val Lys Asp Leu Val Val Asn Thr Trp Asp Ser
 115 120 125
 Leu Lys Asp Phe Asn Phe His Asn Thr Tyr Phe Arg Ala Ile Gly Lys
 130 135 140
 Phe Gly Val Gln Phe Arg Thr Ile Val Leu Tyr His Lys Val Asp Val
 145 150 155 160
 Glu Ile Gly Met Lys Ile Phe Leu Thr Pro Glu Arg Arg Ser Leu Phe
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 Glu Arg Ser Phe Leu Phe Phe Val Ser His Ser Trp His Phe
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 ttt gta gaa ggt cca agc gat aag gtg ttt tta gaa gtt tat ctg tat 102
 Phe Val Glu Gly Pro Ser Asp Lys Val Phe Leu Glu Val Tyr Leu Tyr
 10 15 20
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 Phe Leu Glu Arg Phe Pro Ile Lys Asn Phe Lys Val Gln Asn Val Asp
 25 30 35 40
 gga aaa gat aac ctg tct aaa cga ttg ctt gaa att gaa aaa tac gat 198
 Gly Lys Asp Asn Leu Ser Lys Arg Leu Leu Glu Ile Glu Lys Tyr Asp
 45 50 55
 aaa aca ctt atc att ttt gat gcg gat aaa gac tat gag agt aat aaa 246
 Lys Thr Leu Ile Ile Phe Asp Ala Asp Lys Asp Tyr Glu Ser Asn Lys
 60 65 70

95	100	105	
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cat ggc gat cat tct gat atg tat tta agc agg gat tct ggt tgg ata His Gly Asp His Ser Asp Met Tyr Leu Ser Arg Asp Ser Gly Trp Ile 125 130 135			494
agt tta tgc aca tgc aac ccc caa gaa gct tat gat ttc act tta atg Ser Leu Cys Thr Cys Asn Pro Gln Glu Ala Tyr Asp Phe Thr Leu Met 140 145 150 155			542
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cat tcc ctt ttg gat ttt gat aaa ccg gta agc tat ggc gcg caa gct His Ser Leu Leu Asp Phe Asp Lys Pro Val Ser Tyr Gly Ala Gln Ala 205 210 215			734
gaa gaa gaa tgg cat tat gag cat aaa gcc caa ctc cac cat gcc atc Glu Glu Glu Trp His Tyr Glu His Lys Ala Gln Leu His His Ala Ile 220 225 230 235			782
atg agc gcg tct tct gtg att gaa gaa gtg ttc aat gat ttc gct aaa Met Ser Ala Ser Ser Val Ile Glu Glu Val Phe Asn Asp Phe Ala Lys 240 245 250			830
ctc aca ggc agg caa tac cat tta acc aaa act ttc cag cta gaa gac Leu Thr Gly Arg Gln Tyr His Leu Thr Lys Thr Phe Gln Leu Glu Asp 255 260 265			878
gct gaa atc gct atc ttt gcg tta ggc act act tat gaa tca gcg atc Ala Glu Ile Ala Ile Phe Ala Leu Gly Thr Thr Tyr Glu Ser Ala Ile 270 275 280			926
gta gcg gct aaa gaa atg cgt aaa aaa ggc att aag gcc gcc gtg gct Val Ala Ala Lys Glu Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala 285 290 295			974
acc atc cat tcc ttg cgc ccc ttc cct tat gaa aga tta ggg cag gat Thr Ile His Ser Leu Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp 300 305 310 315			1022
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Gly	Thr	Met	Gly	Ala	Met	Phe	Asn	Glu	Val	Thr	Ser	Ala	Val	Tyr	Gln		
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Thr	Gln	Gly	Thr	Lys	His	Pro	Val	Val	Ser	Asn	Tyr	Ile	Tyr	Gly	Leu		
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ggc	gaa	agg	gat	atg	acg	atc	gcg	cat	tta	tgc	gaa	att	ttt	gaa	gaa	1214	
Gly	Glu	Arg	Asp	Met	Thr	Ile	Ala	His	Leu	Cys	Glu	Ile	Phe	Glu	Glu		
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Ile	Asn	Glu	Asp	Ala	Leu	Lys	Gly	Thr	Leu	Thr	His	Pro	Thr	Gln	Gln		
380					385				390						395		
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Phe	Val	Gly	Leu	His	Gly	Pro	Lys	Met	Ser	Phe	Phe						
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Phe	Lys	Asp	Asn	Gly	Tyr	Val	Asp	Gly	Glu	Phe	Val	Leu	Val	Glu	Ser		
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Arg	Val	Ser	Thr	Ala	Thr	Ser	Ser	Gln	Gly	Leu	Ala	Leu	Met	Val	Glu		
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Val	Leu	Tyr	Gln	Ala	Ser	Gly	Met	Arg	Leu	Pro	Ile	Val	Leu	Asn	Leu		
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Val	Asn	Arg	Ala	Leu	Ala	Ala	Pro	Leu	Asn	Ile	His	Gly	Asp	His	Ser		
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Asp	Met	Tyr	Leu	Ser	Arg	Asp	Ser	Gly	Trp	Ile	Ser	Leu	Cys	Thr	Cys		
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Leu	Cys	Ser	His	Thr	Val	Gln	Asn	Val	Arg	Pro	Leu	Ser	Asp	Ala	Val		
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Ala	Tyr	Gln	Phe	Val	Gly	Glu	Tyr	Gln	Thr	Lys	His	Ser	Leu	Leu	Asp		
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Phe	Asp	Lys	Pro	Val	Ser	Tyr	Gly	Ala	Gln	Ala	Glu	Glu	Glu	Trp	His		
	210					215					220						
Tyr	Glu	His	Lys	Ala	Gln	Leu	His	His	Ala	Ile	Met	Ser	Ala	Ser	Ser		
	225				230					235					240		
Val	Ile	Glu	Glu	Val	Phe	Asn	Asp	Phe	Ala	Lys	Leu	Thr	Gly	Arg	Gln		
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Tyr His Leu Thr Lys Thr Phe Gln Leu Glu Asp Ala Glu Ile Ala Ile
 260 265 270
 Phe Ala Leu Gly Thr Thr Tyr Glu Ser Ala Ile Val Ala Ala Lys Glu
 275 280 285
 Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala Thr Ile His Ser Leu
 290 295 300
 Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp Leu Lys Asn Leu Lys
 305 310 315 320
 Ala Leu Ala Ile Leu Asp Lys Ser Ser Pro Ala Gly Thr Met Gly Ala
 325 330 335
 Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln Thr Gln Gly Thr Lys
 340 345 350
 His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu Gly Glu Arg Asp Met
 355 360 365
 Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu Ile Asn Glu Asp Ala
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 Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu
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 act aaa gtg gat tac act ttt ttt aat aaa aag gtg gtt tcg ccc atc 144
 Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile
 35 40 45
 aaa cgc tat gcg gat aga tcg gcg ttt tat ctg ggg ctt ggg tat caa 192
 Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln
 50 55 60
 tta ggg agc att cag cac aac tct agc aac ttg aat tta tcc cag caa 240
 Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln
 65 70 75 80
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 Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe
 85 90 95
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 Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys
 100 105 110

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gcg	gtt	atc	cat	ttg	gct	aat	ggg	gaa	aat	gtt	gcg	tta	gat	ttt	aga	343			
Ala	Val	Ile	His	Leu	Ala	Asn	Gly	Glu	Asn	Val	Ala	Leu	Asp	Phe	Arg				
90								95				100							
gaa	aaa	gcc	ccc	tta	aaa	gcc	act	aaa	aac	atg	ttt	tta	gac	aag	caa	391			
Glu	Lys	Ala	Pro	Leu	Lys	Ala	Thr	Lys	Asn	Met	Phe	Leu	Asp	Lys	Gln				
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Gly	Asn	Val	Val	Pro	Lys	Leu	Ser	Glu	Asp	Gly	Tyr	Leu	Ala	Ala	Gly				
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Val	Pro	Gly	Thr	Val	Ala	Gly	Met	Glu	Ala	Met	Leu	Lys	Lys	Tyr	Gly				
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act	aaa	aaa	cta	tcg	caa	ctc	att	gat	cct	gcc	att	aaa	ttg	gct	gaa	535			
Thr	Lys	Lys	Leu	Ser	Gln	Leu	Ile	Asp	Pro	Ala	Ile	Lys	Leu	Ala	Glu				
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Asn	Gly	Tyr	Ala	Ile	Ser	Gln	Arg	Gln	Ala	Glu	Thr	Leu	Lys	Glu	Ala				
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Arg	Glu	Arg	Phe	Leu	Lys	Tyr	Ser	Ser	Ser	Lys	Lys	Tyr	Phe	Phe	Lys				
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aaa	ggc	cat	ctt	gat	tat	caa	gaa	ggg	gat	ttg	ttt	gtc	caa	aaa	gat	679			
Lys	Gly	His	Leu	Asp	Tyr	Gln	Glu	Gly	Asp	Leu	Phe	Val	Gln	Lys	Asp				
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Ser	Pro	Pro	Ser	Ser	Gly	Gly													

Met	Glu	Asn	Ala	Asp	Leu	Ser	Ala	Leu	Gly	Tyr	Gly	Ala	Ser	Lys	Asn	
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Ile	His	Ile	Ala	Ala	Glu	Ala	Met	Arg	Gln	Ala	Tyr	Ala	Asp	Arg	Ser	
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Val	Tyr	Met	Gly	Asp	Ala	Asp	Phe	Val	Ser	Val	Pro	Val	Asp	Lys	Leu	
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Ile	Asn	Lys	Ala	Tyr	Ala	Lys	Lys	Ile	Phe	Asp	Thr	Ile	Gln	Pro	Asp	
	345					350				355						
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Thr	Val	Thr	Pro	Ser	Ser	Gln	Ile	Lys	Pro	Gly	Met	Gly	Gln	Leu	His	
360					365				370						375	
gag	ggg	agc	aat	acc	acg	cat	tat	tct	gta	gcg	gac	agg	tgg	ggg	aat	1207
Glu	Gly	Ser	Asn	Thr	Thr	His	Tyr	Ser	Val	Ala	Asp	Arg	Trp	Gly	Asn	
			380						385					390		
gca	gtc	agc	gtt	act	tac	acc	att	aac	gct	tct	tat	gga	agc	gct	gcc	1255
Ala	Val	Ser	Val	Thr	Tyr	Thr	Ile	Asn	Ala	Ser	Tyr	Gly	Ser	Ala	Ala	
			395					400					405			
agt	att	gat	ggg	gca	gga	ttt	tta	ttg	aac	aat	gaa	atg	gat	gat	ttt	1303
Ser	Ile	Asp	Gly	Ala	Gly	Phe	Leu	Leu	Asn	Asn	Glu	Met	Asp	Asp	Phe	
		410					415					420				
tcc	atc	aag	cca	ggg	aat	ccc	aat	ctc	tat	ggg	tta	gta	ggg	ggc	gat	1351
Ser	Ile	Lys	Pro	Gly	Asn	Pro	Asn	Leu	Tyr	Gly	Leu	Val	Gly	Gly	Asp	
		425				430					435					
gcg	aat	gcg	att	gaa	gcc	aat	aag	cgc	cct	tta	agc	tcc	atg	tcg	cct	1399
Ala	Asn	Ala	Ile	Glu	Ala	Asn	Lys	Arg	Pro	Leu	Ser	Ser	Met	Ser	Pro	
440					445				450						455	
acg	att	gtg	ttg	aaa	aac	aat	aag	gtt	ttt	ttg	gtg	gtg	gga	agc	cct	1447
Thr	Ile	Val	Leu	Lys	Asn	Asn	Lys	Val	Phe	Leu	Val	Val	Gly	Ser	Pro	
				460					465					470		
gga	ggg	tct	agg	att	atc	act	acg	gtg	ctg	caa	gtg	att	tct	aat	gtc	1495
Gly	Gly	Ser	Arg	Ile	Ile	Thr	Thr	Val	Leu	Gln	Val	Ile	Ser	Asn	Val	
			475					480					485			
att	gat	tat	aat	atg	aat	att	tct	gaa	gcg	gtt	tca	gcc	cca	aga	ttt	1543
Ile	Asp	Tyr	Asn	Met	Asn	Ile	Ser	Glu	Ala	Val	Ser	Ala	Pro	Arg	Phe	
		490					495					500				
cac	atg	caa	tgg	ctc	cct	gat	gaa	tta	agg	att	gaa	aag	ttt	ggc	atg	1591
His	Met	Gln	Trp	Leu	Pro	Asp	Glu	Leu	Arg	Ile	Glu	Lys	Phe	Gly	Met	
	505					510					515					
ccc	gct	gat	gtg	aaa	gac	aac	ctc	act	aaa	atg	ggc	tat	caa	atc	gtt	1639
Pro	Ala	Asp	Val	Lys	Asp	Asn	Leu	Thr	Lys	Met	Gly	Tyr	Gln	Ile	Val	
520					525					530					535	

act aag ccg gtc atg ggt gat gtg aat gcg atc caa gtt ttg cct aaa 1687
 Thr Lys Pro Val Met Gly Asp Val Asn Ala Ile Gln Val Leu Pro Lys
 540 545 550

act aaa ggg agc gtt ttc tat ggt tca acg gat cca agg aaa gaa ttt 1735
 Thr Lys Gly Ser Val Phe Tyr Gly Ser Thr Asp Pro Arg Lys Glu Phe
 555 560 565

taattcttttg tcatatacag gtttttaatc ctatttagcc ttatttttttg ggatggaggg 1795
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 <213> Helicobacter pylori

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 Lys Asn Thr Lys Val Gly Leu Ala Leu Ser Ser His Pro Leu Ala Ser
 35 40 45
 Glu Ile Gly Gln Lys Val Leu Glu Glu Gly Gly Asn Ala Ile Asp Ala
 50 55 60
 Ala Val Ala Ile Gly Phe Ala Leu Ala Val Val His Pro Ala Ala Gly
 65 70 75 80
 Asn Ile Gly Gly Gly Gly Phe Ala Val Ile His Leu Ala Asn Gly Glu
 85 90 95
 Asn Val Ala Leu Asp Phe Arg Glu Lys Ala Pro Leu Lys Ala Thr Lys
 100 105 110
 Asn Met Phe Leu Asp Lys Gln Gly Asn Val Val Pro Lys Leu Ser Glu
 115 120 125
 Asp Gly Tyr Leu Ala Ala Gly Val Pro Gly Thr Val Ala Gly Met Glu
 130 135 140
 Ala Met Leu Lys Lys Tyr Gly Thr Lys Lys Leu Ser Gln Leu Ile Asp
 145 150 155 160
 Pro Ala Ile Lys Leu Ala Glu Asn Gly Tyr Ala Ile Ser Gln Arg Gln
 165 170 175
 Ala Glu Thr Leu Lys Glu Ala Arg Glu Arg Phe Leu Lys Tyr Ser Ser
 180 185 190
 Ser Lys Lys Tyr Phe Phe Lys Lys Gly His Leu Asp Tyr Gln Glu Gly
 195 200 205
 Asp Leu Phe Val Gln Lys Asp Leu Ala Lys Thr Leu Asn Gln Ile Lys
 210 215 220
 Thr Leu Gly Ala Lys Gly Phe Tyr Gln Gly Gln Val Ala Glu Leu Ile
 225 230 235 240
 Glu Lys Asp Met Lys Lys Asn Gly Gly Ile Ile Thr Lys Glu Asp Leu
 245 250 255
 Ala Ser Tyr Asn Val Lys Trp Arg Lys Pro Val Val Gly Ser Tyr Arg
 260 265 270
 Gly Tyr Lys Ile Ile Ser Met Ser Pro Pro Ser Ser Gly Gly Thr His
 275 280 285
 Leu Ile Gln Ile Leu Asn Val Met Glu Asn Ala Asp Leu Ser Ala Leu
 290 295 300
 Gly Tyr Gly Ala Ser Lys Asn Ile His Ile Ala Ala Glu Ala Met Arg
 305 310 315 320
 Gln Ala Tyr Ala Asp Arg Ser Val Tyr Met Gly Asp Ala Asp Phe Val
 325 330 335

Ser Val Pro Val Asp Lys Leu Ile Asn Lys Ala Tyr Ala Lys Lys Ile
 340 345 350
 Phe Asp Thr Ile Gln Pro Asp Thr Val Thr Pro Ser Ser Gln Ile Lys
 355 360 365
 Pro Gly Met Gly Gln Leu His Glu Gly Ser Asn Thr Thr His Tyr Ser
 370 375 380
 Val Ala Asp Arg Trp Gly Asn Ala Val Ser Val Thr Tyr Thr Ile Asn
 385 390 395 400
 Ala Ser Tyr Gly Ser Ala Ala Ser Ile Asp Gly Ala Gly Phe Leu Leu
 405 410 415
 Asn Asn Glu Met Asp Asp Phe Ser Ile Lys Pro Gly Asn Pro Asn Leu
 420 425 430
 Tyr Gly Leu Val Gly Gly Asp Ala Asn Ala Ile Glu Ala Asn Lys Arg
 435 440 445
 Pro Leu Ser Ser Met Ser Pro Thr Ile Val Leu Lys Asn Asn Lys Val
 450 455 460
 Phe Leu Val Val Gly Ser Pro Gly Gly Ser Arg Ile Ile Thr Thr Val
 465 470 475 480
 Leu Gln Val Ile Ser Asn Val Ile Asp Tyr Asn Met Asn Ile Ser Glu
 485 490 495
 Ala Val Ser Ala Pro Arg Phe His Met Gln Trp Leu Pro Asp Glu Leu
 500 505 510
 Arg Ile Glu Lys Phe Gly Met Pro Ala Asp Val Lys Asp Asn Leu Thr
 515 520 525
 Lys Met Gly Tyr Gln Ile Val Thr Lys Pro Val Met Gly Asp Val Asn
 530 535 540
 Ala Ile Gln Val Leu Pro Lys Thr Lys Gly Ser Val Phe Tyr Gly Ser
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 Thr Asp Pro Arg Lys Glu Phe
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 Met Gln Asn His Asp Leu Glu Ser Ile Lys Gln Ala
 1 5 10
 gct ttg att gaa tat gaa gtg aga gaa caa ggc tct agt att gtg cta 159
 Ala Leu Ile Glu Tyr Glu Val Arg Glu Gln Gly Ser Ser Ile Val Leu
 15 20 25
 gac agc aat att tcc aaa gag cct tta gag ttt att ata ggc act aat 207
 Asp Ser Asn Ile Ser Lys Glu Pro Leu Glu Phe Ile Ile Gly Thr Asn
 30 35 40
 caa atc ata gca ggg tta gaa aag gcg gta tta aag gct caa att ggc 255
 Gln Ile Ile Ala Gly Leu Glu Lys Ala Val Leu Lys Ala Gln Ile Gly
 45 50 55 60
 gag tgg gaa gag gtt gtc atc gcc cca gag gaa gct tat ggg gtt tat 303

50 55 60
 Leu Thr Thr Asn Ile His Gln Leu Pro Lys Pro Ile Ala Thr Arg Leu
 65 70 75 80
 Phe Asn Ser Ser Ser Asn Thr Gly Ile Cys Ala Cys Asn Cys Ser Phe
 85 90 95
 Ser Ala Cys Phe Ser Phe Cys Asn Cys Phe Ala Asn Ala Ser Asn Ser
 100 105 110

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 <212> DNA
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 Met Gly Phe Phe Lys Leu Lys
 1 5

 gaa cac aac act aac att gcc acc gag ttt aga gcg ggt tta acg acc 102
 Glu His Asn Thr Asn Ile Ala Thr Glu Phe Arg Ala Gly Leu Thr Thr
 10 15 20

 ttt atc acc atg att tac atc gtg ccc tta aac gct ctt atc ctt tct 150
 Phe Ile Thr Met Ile Tyr Ile Val Pro Leu Asn Ala Leu Ile Leu Ser
 25 30 35

 caa gcc aac atg cct tat gaa gcc ctt tta agt gca acg gcc att atc 198
 Gln Ala Asn Met Pro Tyr Glu Ala Leu Leu Ser Ala Thr Ala Ile Ile
 40 45 50 55

 act atc tta tcg agc gtg ttt aac gga ttg tgg gca aac acc cct atc 246
 Thr Ile Leu Ser Ser Val Phe Asn Gly Leu Trp Ala Asn Thr Pro Ile
 60 65 70

 gct atg agc gtg ggc tta ggg ctg tca gct tat ttt agc ttc ggg ttg 294
 Ala Met Ser Val Gly Leu Gly Leu Ser Ala Tyr Phe Ser Phe Gly Leu
 75 80 85

 gtt caa ggg tta aaa ctc cct tgg cag agc gct tta ggc atc gta gcg 342
 Val Gln Gly Leu Lys Leu Pro Trp Gln Ser Ala Leu Gly Ile Val Ala
 90 95 100

 ctc tcg gga gcg att ttt gtg att ttg tct ttc act aaa ttt aga agt 390
 Leu Ser Gly Ala Ile Phe Val Ile Leu Ser Phe Thr Lys Phe Arg Ser
 105 110 115

 tgg gtc atg cga agc att cct agc gat tta agg cgt gcg gtg agt gcg 438
 Trp Val Met Arg Ser Ile Pro Ser Asp Leu Arg Arg Ala Val Ser Ala
 120 125 130 135

 ggg ata ggg gct ttt atc gcg ttt att ggc ctt aaa gaa atg cat atc 486
 Gly Ile Gly Ala Phe Ile Ala Phe Ile Gly Leu Lys Glu Met His Ile
 140 145 150

 gtc gtt acc cat aar gct acg ctt gta acc tta ggc gat ttt ggc gat 534

Val	Val	Thr	His	Xaa	Ala	Thr	Leu	Val	Thr	Leu	Gly	Asp	Phe	Gly	Asp		
			155					160					165				
ccg	cat	gtg	tta	ttg	ggg	gtt	gtg	ggg	atc	att	cta	act	ttc	gcg	ctc	582	
Pro	His	Val	Leu	Leu	Gly	Val	Val	Gly	Ile	Ile	Leu	Thr	Phe	Ala	Leu		
		170					175					180					
tac	acg	ctc	aaa	atc	agg	ggt	tct	ttc	att	ata	gcg	gtc	tta	atc	act	630	
Tyr	Thr	Leu	Lys	Ile	Arg	Gly	Ser	Phe	Ile	Ile	Ala	Val	Leu	Ile	Thr		
	185					190					195						
tcc	att	ctc	gca	tgg	gtt	tta	aag	cta	gcc	cct	tac	cct	agc	gag	ttt	678	
Ser	Ile	Leu	Ala	Trp	Val	Leu	Lys	Leu	Ala	Pro	Tyr	Pro	Ser	Glu	Phe		
200					205					210					215		
ttt	tcc	atg	ccc	gct	agc	att	ggc	cct	atc	gcc	ttt	caa	tta	gac	ttt	726	
Phe	Ser	Met	Pro	Ala	Ser	Ile	Gly	Pro	Ile	Ala	Phe	Gln	Leu	Asp	Phe		
				220					225					230			
aag	ggc	att	ttt	ttt	gat	gcg	agt	ggg	gct	ttc	act	tta	gcg	tta	gtg	774	
Lys	Gly	Ile	Phe	Phe	Asp	Ala	Ser	Gly	Ala	Phe	Thr	Leu	Ala	Leu	Val		
			235					240					245				
cca	gtt	att	atc	act	ttt	ttt	gta	acc	gat	ttg	ttt	gat	tct	tta	ggc	822	
Pro	Val	Ile	Ile	Thr	Phe	Phe	Val	Thr	Asp	Leu	Phe	Asp	Ser	Leu	Gly		
		250					255					260					
acg	ctt	gca	ggg	att	ggc	cac	aag	act	gat	ttt	ttc	aat	gat	gaa	gaa	870	
Thr	Leu	Ala	Gly	Ile	Gly	His	Lys	Thr	Asp	Phe	Phe	Asn	Asp	Glu	Glu		
	265					270					275						
aaa	aac	aag	gaa	ttg	gaa	aag	act	ttg	gaa	gcg	gat	gcg	gtg	gct	tct	918	
Lys	Asn	Lys	Glu	Leu	Glu	Lys	Thr	Leu	Glu	Ala	Asp	Ala	Val	Ala	Ser		
280					285				290						295		
tta	ggg	agc	gcg	gtg	gtg	ggc	gtt	tct	act	acg	acc	gct	ttt	ata	gag	966	
Leu	Gly	Ser	Ala	Val	Val	Gly	Val	Ser	Thr	Thr	Thr	Ala	Phe	Ile	Glu		
				300					305					310			
agc	gcg	agt	ggg	gtt	gaa	gag	ggg	ggc	cgc	aca	ggg	ctt	aca	gcg	gtt	1014	
Ser	Ala	Ser	Gly	Val	Glu	Glu	Gly	Gly	Arg	Thr	Gly	Leu	Thr	Ala	Val		
			315					320					325				
ttt	acc	gga	tta	ttt	ttt	gtt	tta	acg	ctc	ttt	tgc	ttg	cct	ctt	tta	1062	
Phe	Thr	Gly	Leu	Phe	Phe	Val	Leu	Thr	Leu	Phe	Cys	Leu	Pro	Leu	Leu		
		330					335					340					
aaa	gct	att	cct	agc	aat	gcg	att	tat	ccg	gtg	ctg	gtg	gta	gta	ggg	1110	
Lys	Ala	Ile	Pro	Ser	Asn	Ala	Ile	Tyr	Pro	Val	Leu	Val	Val	Val	Gly		
	345					350					355						
gtt	ttg	atg	ttt	agc	gtg	tta	gag	ggg	gtg	aat	ttt	aaa	gac	atg	gcc	1158	
Val	Leu	Met	Phe	Ser	Val	Leu	Glu	Gly	Val	Asn	Phe	Lys	Asp	Met	Ala		
360					365					370					375		
att	agc	gtt	tcc	act	ttt	tta	acc	gtg	gtg	atg	atg	ccc	tta	acc	ttc	1206	
Ile	Ser	Val	Ser	Thr	Phe	Leu	Thr	Val	Val	Met	Met	Pro	Leu	Thr	Phe		
				380					385					390			

tcc att gcc gat ggc tta gcc ttt ggc ttt ttg tct tat agt atc atc	1254
Ser Ile Ala Asp Gly Leu Ala Phe Gly Phe Leu Ser Tyr Ser Ile Ile	
395 400 405	
aaa ttg gtt caa aaa gac ttc aaa gca ctc aat tca ggc att atc att	1302
Lys Leu Val Gln Lys Asp Phe Lys Ala Leu Asn Ser Gly Ile Ile Ile	
410 415 420	
ctc tgc atc att tct gtt tct gta ttt atc ttt cgt taagctcttt	1348
Leu Cys Ile Ile Ser Val Ser Val Phe Ile Phe Arg	
425 430 435	
taaaggggct ttgcattttt tactcatttc atgcctcttt ttctttatatt agacagatta	1408
ttatcttaaaa ataattgtaa tatcattatt at	1440

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<210> 146
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<212> PRT
<213> Helicobacter pylori
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Leu	Asn	Ala	Leu	Ile	Leu	Ser	Gln 40	Ala	Asn	Met	Pro	Tyr 45	Glu	Ala	Leu
Leu	Ser 50	Ala	Thr	Ala	Ile	Ile 55	Thr	Ile	Leu	Ser	Ser 60	Val	Phe	Asn	Gly
Leu 65	Trp	Ala	Asn	Thr	Pro 70	Ile	Ala	Met	Ser	Val 75	Gly	Leu	Gly	Leu	Ser 80
Ala	Tyr	Phe	Ser	Phe 85	Gly	Leu	Val	Gln	Gly 90	Leu	Lys	Leu	Pro	Trp 95	Gln
Ser	Ala	Leu	Gly 100	Ile	Val	Ala	Leu	Ser 105	Gly	Ala	Ile	Phe	Val 110	Ile	Leu
Ser	Phe	Thr 115	Lys	Phe	Arg	Ser	Trp 120	Val	Met	Arg	Ser	Ile 125	Pro	Ser	Asp
Leu	Arg 130	Arg	Ala	Val	Ser	Ala 135	Gly	Ile	Gly	Ala	Phe 140	Ile	Ala	Phe	Ile
Gly 145	Leu	Lys	Glu	Met 150	His	Ile	Val	Val	Thr 155	His	Xaa	Ala	Thr	Leu	Val 160
Thr	Leu	Gly	Asp	Phe 165	Gly	Asp	Pro	His	Val 170	Leu	Leu	Gly	Val	Val 175	Gly
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Ala	Pro 210	Tyr	Pro	Ser	Glu	Phe 215	Phe	Ser	Met	Pro	Ala 220	Ser	Ile	Gly	Pro
Ile 225	Ala	Phe	Gln	Leu	Asp 230	Phe	Lys	Gly	Ile	Phe 235	Asp	Ala	Ser	Gly 240	
Ala	Phe	Thr	Leu	Ala 245	Leu	Val	Pro	Val	Ile 250	Ile	Thr	Phe	Phe	Val 255	Thr
Asp	Leu	Phe	Asp 260	Ser	Leu	Gly	Thr	Leu 265	Ala	Gly	Ile	Gly	His 270	Lys	Thr
Asp	Phe	Phe 275	Asn	Asp	Glu	Glu	Lys 280	Asn	Lys	Glu	Leu	Glu 285	Lys	Thr	Leu
Glu	Ala 290	Asp	Ala	Val	Ala	Ser 295	Leu	Gly	Ser	Ala	Val 300	Val	Gly	Val	Ser

Thr Thr Thr Ala Phe Ile Glu Ser Ala Ser Gly Val Glu Glu Gly Gly
 305 310 315 320
 Arg Thr Gly Leu Thr Ala Val Phe Thr Gly Leu Phe Phe Val Leu Thr
 325 330 335
 Leu Phe Cys Leu Pro Leu Leu Lys Ala Ile Pro Ser Asn Ala Ile Tyr
 340 345 350
 Pro Val Leu Val Val Val Gly Val Leu Met Phe Ser Val Leu Glu Gly
 355 360 365
 Val Asn Phe Lys Asp Met Ala Ile Ser Val Ser Thr Phe Leu Thr Val
 370 375 380
 Val Met Met Pro Leu Thr Phe Ser Ile Ala Asp Gly Leu Ala Phe Gly
 385 390 395 400
 Phe Leu Ser Tyr Ser Ile Ile Lys Leu Val Gln Lys Asp Phe Lys Ala
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 Ile Phe Arg
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 <212> DNA
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 Met Thr Pro His Ile Asn Ala Lys Ile Gly Asp Phe Tyr Pro Gln
 1 5 10 15
 tgc ctt tta tgc ggc gat ccc tta agg gtg agc tac att gca aaa aaa 158
 Cys Leu Leu Cys Gly Asp Pro Leu Arg Val Ser Tyr Ile Ala Lys Lys
 20 25 30
 ttc tta caa gac gcc aaa gag atc acg aat gtg cgt aac atg cta ggc 206
 Phe Leu Gln Asp Ala Lys Glu Ile Thr Asn Val Arg Asn Met Leu Gly
 35 40 45
 ttt agc ggg aag tat aag ggt agg ggg att tct tta atg ggg cat ggc 254
 Phe Ser Gly Lys Tyr Lys Gly Arg Gly Ile Ser Leu Met Gly His Gly
 50 55 60
 atg ggc att gcg tca tgc acg att tat gta acc gaa ctc att aaa acc 302
 Met Gly Ile Ala Ser Cys Thr Ile Tyr Val Thr Glu Leu Ile Lys Thr
 65 70 75
 tat cag gtt aaa gag ctt tta agg att ggc act tgc ggg gcg att agc 350
 Tyr Gln Val Lys Glu Leu Leu Arg Ile Gly Thr Cys Gly Ala Ile Ser
 80 85 90 95
 cca aaa gtt ggc ctg aaa gac att atc atg gcg acg ggg gct tca acg 398
 Pro Lys Val Gly Leu Lys Asp Ile Ile Met Ala Thr Gly Ala Ser Thr
 100 105 110
 gat tct aaa acc aat cgg gtg cgt ttt tta aac cac gat ttg agc gca 446

Ser Phe Glu Thr His Ala Phe Asp Leu Met Ala Lys Tyr Asn His Leu
165 170 175
Ala Ile Glu Met Glu Ala Ala Gly Leu Tyr Ala Thr Ala Met Glu Leu
180 185 190
Asn Ala Lys Ala Leu Cys Leu Cys Ser Val Ser Asp His Leu Ile Thr
195 200 205
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210 215 220
Ile Ile Leu Ala Leu Glu Met Met Ser
225 230

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<212> DNA
<213> Helicobacter pylori

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<222> (79)...(1407)

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Met Phe Lys Lys Ile Phe Pro Leu Ala Leu Val
1 5 10
tca tcg ttg cgg ttt ttg ggg ctt ttt att gtt ttg ccg gtc att agt 159
Ser Ser Leu Arg Phe Leu Gly Leu Phe Ile Val Leu Pro Val Ile Ser
15 20 25
ttg tat gcg gat agt ttc cat tca agc agt ccc tta ctc gtg ggg ttg 207
Leu Tyr Ala Asp Ser Phe His Ser Ser Ser Pro Leu Leu Val Gly Leu
30 35 40
gct gtg ggc gga gcg tat ctt acg caa att gtt ttt caa acc ccc atg 255
Ala Val Gly Gly Ala Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met
45 50 55
ggc att ctt agc gat aag ata ggc cgt aaa gtg gtg gtt atg gtg tgc 303
Gly Ile Leu Ser Asp Lys Ile Gly Arg Lys Val Val Val Met Val Cys
60 65 70 75
ttg ctg ttg ttt tta gcc ggc tcg tta gtg tgc ttt ata gcg aat gat 351
Leu Leu Leu Phe Leu Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp
80 85 90
att gtt tgg ctc gtt ata ggg cgc ttc att caa ggc atg ggg gct tta 399
Ile Val Trp Leu Val Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu
95 100 105
ggg ggg gtt att agt gcg atg gtg gcg gat gaa gtg aaa gaa gaa gag 447
Gly Gly Val Ile Ser Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu
110 115 120
cgc acc aaa gcc atg gcc atc atg gga gcg ttt att ttc att agc ttc 495
Arg Thr Lys Ala Met Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe
125 130 135
act ata agc atg gcg att ggc cct ggg gtt gta gcg ttt ttg ggg ggg 543

Thr 140	Ile	Ser	Met	Ala	Ile 145	Gly	Pro	Gly	Val	Val 150	Ala	Phe	Leu	Gly	Gly 155	
gca Ala	aaa Lys	tgg Trp	ctc Leu	ttt Phe 160	tta Leu	ctc Leu	acg Thr	gcg Ala	atc Ile 165	tta Leu	act Thr	tta Leu	ttg Leu	agt Ser 170	tta Leu	591
ttg Leu	atg Met	ctt Leu	tta Leu 175	aaa Lys	gtc Val	aaa Lys	gac Asp	gcc Ala 180	cct Pro	aaa Lys	att Ile	tct Ser	tac Tyr 185	cag Gln	atc Ile	639
aaa Lys	aac Asn 190	ata Ile	aaa Lys	gct Ala	tac Tyr	caa Gln	ccc Pro 195	aac Asn	tct Ser	aaa Lys	gcc Ala 200	ttg Leu	tat Tyr	ctt Leu	ttg Leu	687
tat Tyr 205	cta Leu	agc Ser	tct Ser	ttt Phe	ttt Phe 210	gaa Glu	aaa Lys	gcg Ala	ttc Phe	atg Met 215	acg Thr	ctt Leu	att Ile	ttt Phe	gtg Val	735
ctg Leu 220	atc Ile	cct Pro	tta Leu	gcc Ala 225	tta Leu	gtg Val	aat Asn	gaa Glu	ttt Phe 230	cat His	aaa Lys	gat Asp	gaa Glu	agc Ser	ttt Phe 235	783
tta Leu	atc Ile	ttg Leu	gtg Val 240	tat Tyr	gtg Val	cct Pro	gga Gly	gcc Ala	tta Leu 245	tta Leu	ggg Gly	gtc Val	tta Leu	agc Ser 250	atg Met	831
gga Gly	ata Ile	gcg Ala	agc Ser 255	gtt Val	atg Met	gct Ala	gaa Glu	aaa Lys 260	tac Tyr	aac Asn	aag Lys	cct Pro	aaa Lys 265	gga Gly	gtg Val	879
atg Met	ctt Leu	tct Ser 270	ggc Gly	gta Val	tta Leu	ttg Leu	ttt Phe 275	att Ile	gtg Val	agt Ser	tat Tyr	ttg Leu 280	tgc Cys	ttg Leu	ttt Phe	927
tta Leu 285	gcc Ala	gac Asp	tct Ser	agc Ser	ttt Phe 290	tta Leu	ggg Gly	aaa Lys	tat Tyr	tta Leu	tgg Trp 295	ctt Leu	ttt Phe	att Ile	gtt Val	975
ggg Gly 300	gtg Val	gcg Ala	ttt Phe	ttc Phe 305	att Ile	ggt Gly	ttt Phe	gcc Ala 310	acc Thr	tta Leu	gag Glu	cct Pro	atc Ile 315	atg Met		1023
caa Gln	tct Ser	tta Leu	gcg Ala 320	tct Ser	aaa Lys	ttc Phe	gcc Ala	aaa Lys 325	gtg Val	cat His	gaa Glu	aaa Lys	ggc Gly 330	aag Lys	gtt Val	1071
tta Leu	ggg Gly	caa Gln 335	ttc Phe	act Thr	act Thr	ttt Phe	ggc Gly	tat Tyr 340	tta Leu	ggg Gly	agc Ser	ttt Phe 345	gtt Val	ggg Gly	ggc Gly	1119
gtg Val	agc Ser 350	ggg Gly	ggg Gly	ttg Leu	agc Ser	tac Tyr	cat His 355	cat His	tta Leu	ggc Gly	gtt Val 360	tct Ser	aac Asn	aca Thr	agc Ser	1167
ttg Leu	atc Ile 365	gtt Val	gta Val	gct Ala	tta Leu	ggg Gly 370	ctt Leu	att Ile	tgg Trp	ggg Gly 375	cta Leu 380	tcg Ser	ctc Leu	ttt Phe	tta Leu	1215

90				95				100								
ctt	aat	tta	gag	cct	att	ttt	atg	gtg	att	ttc	cct	att	att	agt	ttg	448
Leu	Asn	Leu	Glu	Pro	Ile	Phe	Met	Val	Ile	Phe	Pro	Ile	Ile	Ser	Leu	
105					110					115					120	
ggc	atg	atc	atg	act	tta	gtc	aaa	gat	tat	cgt	aaa	gag	att	ttg	tgg	496
Gly	Met	Ile	Met	Thr	Leu	Val	Lys	Asp	Tyr	Arg	Lys	Glu	Ile	Leu	Trp	
				125					130					135		
ctt	gat	ttg	gtt	ttg	aaa	gtg	ggc	gtt	att	ggg	gaa	ttg	tta	agc	att	544
Leu	Asp	Leu	Val	Leu	Lys	Val	Gly	Val	Ile	Gly	Glu	Leu	Leu	Ser	Ile	
			140						145					150		
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Phe	Gly	Leu	Val	Val	Val	Asp	Gly	Val	Tyr	Ser	His	Gly	Leu	Gly	Met	
		155					160					165				
gat	ttg	att	aaa	gat	tta	ggc	att	ctc	att	gtt	ttt	tta	atc	tta	att	640
Asp	Leu	Ile	Lys	Asp	Leu	Gly	Ile	Leu	Ile	Val	Phe	Leu	Ile	Leu	Ile	
	170					175					180					
atc	gtg	gcg	ttt	caa	atc	ttt	aag	act	ttg	ttt	tgg	tgg	ttc	ccg	cat	688
Ile	Val	Ala	Phe	Gln	Ile	Phe	Lys	Thr	Leu	Phe	Trp	Trp	Phe	Pro	His	
185					190					195					200	
tta	aag	ctt	ttt	gtg	atg	cct	aaa	agc	agt	cag	ttt	aac	caa	gat	gtg	736
Leu	Lys	Leu	Phe	Val	Met	Pro	Lys	Ser	Ser	Gln	Phe	Asn	Gln	Asp	Val	
			205						210					215		
cgt	ttt	tcg	ctc	atg	ctc	ttt	ttt	tcc	tta	gtt	gcg	atc	gtg	gtg	tgg	784
Arg	Phe	Ser	Leu	Met	Leu	Phe	Phe	Ser	Leu	Val	Ala	Ile	Val	Val	Trp	
			220					225					230			
ctc	aaa	ata	gaa	atg	gtt	tta	ggg	gcg	ttt	cta	gca	ggg	tta	gtc	gtt	832
Leu	Lys	Ile	Glu	Met	Val	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Leu	Val	Val	
		235					240					245				
tct	act	ttt	ttc	cct	cat	aaa	tca	gaa	ttg	atc	cac	aag	ctc	aat	gat	880
Ser	Thr	Phe	Phe	Pro	His	Lys	Ser	Glu	Leu	Ile	His	Lys	Leu	Asn	Asp	
	250					255					260					
gtg	ggg	ttt	ggg	ttt	ttt	gtg	cct	ttg	ttt	ttc	atc	cat	gta	ggc	tct	928
Val	Gly	Phe	Gly	Phe	Phe	Val	Pro	Leu	Phe	Phe	Ile	His	Val	Gly	Ser	
265				270						275				280		
act	tta	gac	tta	aaa	tta	gtg	ttt	tta	aac	ccg	cat	ttg	att	ctc	caa	976
Thr	Leu	Asp	Leu	Lys	Leu	Val	Phe	Leu	Asn	Pro	His	Leu	Ile	Leu	Gln	
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ggg	ata	ttg														

Phe Ala Leu Gly Ala Ser Met Pro Leu Thr Phe Leu Val Thr Thr Ala
 330 335 340

gca gta ggc tta aaa gcg caa gcg atc tca caa aac acc tac tac gca 1168
 Ala Val Gly Leu Lys Ala Gln Ala Ile Ser Gln Asn Thr Tyr Tyr Ala
 345 350 355 360

ttg ctc atg gcg gct att ttt gaa ggg gta tta ttc acg att gcg atc 1216
 Leu Leu Met Ala Ala Ile Phe Glu Gly Val Leu Phe Thr Ile Ala Ile
 365 370 375

aaa ata ctc aac aaa aaa gct tgaatgaaag ctttaagcgctc taaatattta 1267
 Lys Ile Leu Asn Lys Lys Ala
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gcgtcgctaa agctgttcgc ttgaacatta ttgaacgcat tctctaagct atcaaagaaa 1327
 cgagggtgca agttttgcat ttcttttaag aaa 1360

<210> 152
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 <212> PRT
 <213> Helicobacter pylori

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 Met Ala Pro Tyr Met Ser Arg Ile Ser Arg Leu Pro Ile Thr Val Val
 20 25 30
 Glu Ile Leu Phe Gly Ser Val Gly Ala Tyr Val Gly Phe Ile Glu Pro
 35 40 45
 Thr Lys Gly Phe Glu Ile Met Ser Glu Ile Gly Phe Leu Phe Leu Met
 50 55 60
 Phe Leu Cys Gly Leu Glu Val Glu Ile Tyr Leu Phe Lys Lys Leu Gly
 65 70 75 80
 Val Ser Leu Leu Lys Arg Ile Phe Ala Tyr Leu Leu Ile Leu Tyr Thr
 85 90 95
 Leu Ser Phe Ile Leu Thr Phe Ser Leu Asn Leu Glu Pro Ile Phe Met
 100 105 110
 Val Ile Phe Pro Ile Ile Ser Leu Gly Met Ile Met Thr Leu Val Lys
 115 120 125
 Asp Tyr Arg Lys Glu Ile Leu Trp Leu Asp Leu Val Leu Lys Val Gly
 130 135 140
 Val Ile Gly Glu Leu Leu Ser Ile Phe Gly Leu Val Val Val Asp Gly
 145 150 155 160
 Val Tyr Ser His Gly Leu Gly Met Asp Leu Ile Lys Asp Leu Gly Ile
 165 170 175
 Leu Ile Val Phe Leu Ile Leu Ile Ile Val Ala Phe Gln Ile Phe Lys
 180 185 190
 Thr Leu Phe Trp Trp Phe Pro His Leu Lys Leu Phe Val Met Pro Lys
 195 200 205
 Ser Ser Gln Phe Asn Gln Asp Val Arg Phe Ser Leu Met Leu Phe Phe
 210 215 220
 Ser Leu Val Ala Ile Val Val Trp Leu Lys Ile Glu Met Val Leu Gly
 225 230 235 240
 Ala Phe Leu Ala Gly Leu Val Val Ser Thr Phe Phe Pro His Lys Ser
 245 250 255
 Glu Leu Ile His Lys Leu Asn Asp Val Gly Phe Gly Phe Phe Val Pro
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[illegible]

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<221> CDS
<222> (115) ... (921)
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-173-

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Phe	Phe	Met	Lys	Lys	Leu	Gly	Ile	Lys	Gly	Gly	Ile	Ala	Ile	Glu	Val			
130						135						140						
gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	aaa	acc	aat	caa	acc	cct	597		
Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	Asn	Gln	Thr	Pro			
					150						155							
atc	cag	cca	aaa	cac	ctc	ccc	aac	tct	aaa	caa	ccc	cac	tct	caa	aga	645		
Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	His	Ser	Gln	Arg			
					165						170							
gga	tca	aaa	gcg	caa	gag	ctt	atc	gct	tat	ttg	caa	aaa	gag	tta	gaa	693		
Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln	Lys	Glu	Leu	Glu			
					180						185							
tct	ctg	ccc	tat	tca	caa	aaa	gct	atc	gct	aaa	caa	gtg	aat	ttt	tac	741		
Ser	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln	Val	Asn	Phe	Tyr			
					195						200							
agg	cca	agt	tct	gtc	gct	tat	tta	gaa	cta	gac	cct	aga	gat	ttt	aag	789		
Arg	Pro	Ser	Ser	Val	Ala	Tyr	Leu	Glu	Leu	Asp	Pro	Arg	Asp	Phe	Lys			
					210						215							
gtt	aca	gaa	gaa	tgg	caa	aaa	gaa	aat	cta	aaa	ata	cgc	tct	aaa	gct	837		
Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile	Arg	Ser	Lys	Ala			
					230						235							
caa	gct	aaa	atg	ctt	gga	aat	gag	aaa	ccc	aca	agc	cca	cct	ttc	aac	885		
Gln	Ala	Lys	Met	Leu	Gly	Asn	Glu	Lys	Pro	Thr	Ser	Pro	Pro	Phe	Asn			
					245						250							
ctc	tca	aag	cct	ttt	gtt	cgt	tca	aaa	aat	att	tgc	tgatgttaat				931		
Leu	Ser	Lys	Pro	Phe	Val	Arg	Ser	Lys	Asn	Ile	Cys							
					260						265							
aaagaaatatag aagcagttgc taatactgaa aagaaagcag aaaaagmggg ttatgggttat																991		
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<210> 154
<211> 269
<212> PRT
<213> Helicobacter pylori
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Met 1																Val 20																Leu 35																Gln 50																Leu 65																Glu 85															
Lys 1																Ala 20																Asp 35																Ile 50																Leu 65																Gln 85															
Arg 5																Leu 20																Gln 35																Tyr 50																Val 65																Ala 85															
Val 5																Thr 20																Asp 35																Ser 50																Gly 65																Glu 85															
Glu 10																His 25																Lys 40																Ile 55																Asp 70																Ala 90															
Lys 10																Cys 30																Ser 45																Leu 60																Arg 75																Asn 95															
His 15																Lys 30																Gln 45																Thr 60																Ile 75																Ala 95															
Pro 15																Lys 30																Ala 45																Ile 60																Arg 75																Asn 95															
Glu 15																Ala 30																Glu 45																Thr 60																Ile 75																Ala 95															
Ser 15																Lys 30																Glu 45																Ser 60																Glu 75																Leu 95															
Val 15																Glu 30																Thr 45																Leu 60																Glu 75																Leu 95															

acg ctt ctg cct gaa aaa tcc acg cgc tta cct aaa agg ttt tgc ctg 152
 Thr Leu Leu Pro Glu Lys Ser Thr Arg Leu Pro Lys Arg Phe Cys Leu
 20 25 30

aaa cgc ccc tgc ttg cct tta atg att tca ctg agc gat ttt aaa ggg 200
 Lys Arg Pro Cys Leu Pro Leu Met Ile Ser Leu Ser Asp Phe Lys Gly
 35 40 45 50

cgt ttg tta gcc cct tta acc gca tta gtg ctg cgg ccg tta tca aaa 248
 Arg Leu Leu Ala Pro Leu Thr Ala Leu Val Leu Arg Pro Leu Ser Lys
 55 60 65

agc aca tcc acg gct tct tgc aac atc ctt ttt tca ttg cgc aca atg 296
 Ser Thr Ser Thr Ala Ser Cys Asn Ile Leu Phe Ser Leu Arg Thr Met
 70 75 80

att tct ggc gct cca agc tcc att aag cgt ttc aag cgt tgg tta cga 344
 Ile Ser Gly Ala Pro Ser Ser Ile Lys Arg Phe Lys Arg Trp Leu Arg
 85 90 95

ttg atg aca cga cga tac aat tca ttc aca tcg ctg act gca aac ttc 392
 Leu Met Thr Arg Arg Tyr Asn Ser Phe Thr Ser Leu Thr Ala Asn Phe
 100 105 110

ccg cca tct agc gcg act aaa ggc ctt aaa tcc ggt ggc aat acc ggt 440
 Pro Pro Ser Ser Ala Thr Lys Gly Leu Lys Ser Gly Gly Asn Thr Gly
 115 120 125 130

aaa acc gtg agc atc atc cat tca ggc cta tta cca gaa ttt aaa aag 488
 Lys Thr Val Ser Ile Ile His Ser Gly Leu Leu Pro Glu Phe Lys Lys
 135 140 145

ctt tct acc act ttc aaa cgc tta atg agt ttt ttc ttt ttc gca tca 536
 Leu Ser Thr Thr Phe Lys Arg Leu Met Ser Phe Phe Phe Phe Ala Ser
 150 155 160

gaa ttg gtg tct ttc act tct tct ttc aaa ctc tgc aat aag gtg atc 584
 Glu Leu Val Ser Phe Thr Ser Ser Phe Lys Leu Cys Asn Lys Val Ile
 165 170 175

aaa tca att tct tct aac aaa tcc ttg atc gct tca ccg ccc att tgc 632
 Lys Ser Ile Ser Ser Asn Lys Ser Leu Ile Ala Ser Pro Pro Ile Cys
 180 185 190

gct aca aag ccc ctg tct tcg tat ctt cgt gag ata ttt tgatactgct 681
 Ala Thr Lys Pro Leu Ser Ser Tyr Leu Arg Glu Ile Phe
 195 200 205

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<210> 158
 <211> 207
 <212> PRT
 <213> Helicobacter pylori

<400> 158
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 Thr Ile Thr Leu Leu Pro Glu Lys Ser Thr Arg Leu Pro Lys Arg Phe

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Ser	Gly	Tyr	Gln	Glu	Val	Ile	Ser	Asp	Pro	Ser	Tyr	Lys	Gly	Gln	Phe			
35			40				45											
gtg	ggt	ttt	agc	atg	cct	gag	att	ggg	ggt	gtg	ggt	gct	aat	tct	aaa	249		
Val	Val	Phe	Ser	Met	Pro	Glu	Ile	Gly	Val	Val	Gly	Ala	Asn	Ser	Lys			
50		55				60								65				
gat	gat	gaa	tcc	ttt	ttt	tca	tgc	gca	ggg	ggt	tta	gcg	cgc	cat	tac	297		
Asp	Asp	Glu	Ser	Phe	Phe	Ser	Cys	Ala	Gly	Val	Leu	Ala	Arg	His	Tyr			
70				75				80										
aac	gaa	ttt	ttt	tct	aac	tca	agg	gcg	gat	ttt	agc	ttg	agc	gct	tat	345		
Asn	Glu	Phe	Phe	Ser	Asn	Ser	Arg	Ala	Asp	Phe	Ser	Leu	Ser	Ala	Tyr			
85			90				95											
ttg	aaa	gag	cgt	ggc	ggt	tta	ggg	ggt	tgt	ggc	ggt	gat	act	agg	agt	393		
Leu	Lys	Glu	Arg	Gly	Val	Leu	Gly	Val	Cys	Gly	Val	Asp	Thr	Arg	Ser			
100		105				110												
ttg	att	aaa	acc	tta	cgc	cat	cat	ggg	tgc	tta	atg	atg	gtc	gct	tcc	441		
Leu	Ile	Lys	Thr	Leu	Arg	His	His	Gly	Cys	Leu	Met	Met	Val	Ala	Ser			
115		120				125												
acg	ata	gag	cat	gac	aaa	aac	aag	ctt	gaa	gaa	att	tta	aaa	aac	gct	489		
Thr	Ile	Glu	His	Asp	Lys	Asn	Lys	Leu	Glu	Glu	Ile	Leu	Lys	Asn	Ala			
130		135				140								145				
cct	aaa	att	tct	cac	tcc	ccc	cta	gtg	tct	agc	ggt	tct	acg	cca	aaa	537		
Pro	Lys	Ile	Ser	His	Ser	Pro	Leu	Val	Ser	Ser	Val	Ser	Thr	Pro	Lys			
150				155				160										
ata	acc	acg	cac	cag	cgt	gcg	act	ttt	gat	ttc	aaa	acc	cta	gat	tac	585		
Ile	Thr	Thr	His	Gln	Arg	Ala	Thr	Phe	Asp	Phe	Lys	Thr	Leu	Asp	Tyr			
165			170				175											
aag	cct	ttt	gat	gaa	aaa	acc	tct	cat	aaa	att	atc	gcg	gtg	tta	gac	633		
Lys	Pro	Phe	Asp	Glu	Lys	Thr	Ser	His	Lys	Ile	Ile	Ala	Val	Leu	Asp			
180		185				190												
ttt	ggg	gct	aag	ggc	aat	att	tta	aac	gag	ctt	caa	aat	gtg	ggg	tta	681		
Phe	Gly	Ala	Lys	Gly	Asn	Ile	Leu	Asn	Glu	Leu	Gln	Asn	Val	Gly	Leu			
195		200				205												
aaa	gcc	ctt	att	tac	ccg	cac	cac	act	aaa	gct	agc	gag	ctg	att	aaa	729		
Lys	Ala	Leu	Ile	Tyr	Pro	His	His	Thr	Lys	Ala	Ser	Glu	Leu	Ile	Lys			
210		215				220								225				
gcc	tat	gaa	aaa	aaa	gaa	att	agc	ggg	att	ttc	ctc	tct	aac	ggg	ccg	777		
Ala	Tyr	Glu	Lys	Lys	Glu	Ile	Ser	Gly	Ile	Phe	Leu	Ser	Asn	Gly	Pro			
230				235				240										
ggc	gat	cct	tta	agc	ttg	cag	caa	gaa	att	ggc	gaa	atc	aaa	caa	ctc	825		
Gly	Asp	Pro	Leu	Ser	Leu	Gln	Gln	Glu	Ile	Gly	Glu	Ile	Lys	Gln	Leu			

Lys Ile Thr Thr His Gln Arg Ala Thr Phe Asp Phe Lys Thr Leu Asp
165 170 175
Tyr Lys Pro Phe Asp Glu Lys Thr Ser His Lys Ile Ile Ala Val Leu
180 185 190
Asp Phe Gly Ala Lys Gly Asn Ile Leu Asn Glu Leu Gln Asn Val Gly
195 200 205
Leu Lys Ala Leu Ile Tyr Pro His His Thr Lys Ala Ser Glu Leu Ile
210 215 220
Lys Ala Tyr Glu Lys Lys Glu Ile Ser Gly Ile Phe Leu Ser Asn Gly
225 230 235 240
Pro Gly Asp Pro Leu Ser Leu Gln Gln Glu Ile Gly Glu Ile Lys Gln
245 250 255
Leu Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln
260 265 270
Leu Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly
275 280 285
His His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val
290 295 300
Glu Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu
305 310 315 320
Glu Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu
325 330 335
Gly Val Arg Tyr Lys Asn Ala Pro Ile Ile Ser Val Gln His His Pro
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Glu Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe
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Val Glu Leu Leu Lys Asp Phe
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<212> DNA
<213> Helicobacter pylori

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Met
1

gat att cgc aac gaa ttt tta caa ttt ttt caa aat aaa ggg cat gcc 166
Asp Ile Arg Asn Glu Phe Leu Gln Phe Phe Gln Asn Lys Gly His Ala
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gtt tat cct agc atg cct tta gtg cct aat gac gct acc ttg ctt ttt 214
Val Tyr Pro Ser Met Pro Leu Val Pro Asn Asp Ala Thr Leu Leu Phe
20 25 30

acc aat gcc ggc atg gtg caa ttt aaa gat att ttt acc ggg att gtg 262
Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile Val
35 40 45

cca cgc cct agc att cct aga gcg gca agc tcg caa ttg tgc atg cgc 310
Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met Arg
50 55 60 65

290	295	300	305	
cat ggg tat tta atg ggc ttg aaa gaa gcg ttt tta tac aaa gtc gtg				1078
His Gly Tyr Leu Met Gly Leu Lys Glu Ala Phe Leu Tyr Lys Val Val	310	315	320	
ggc gtg gtg tgc gag caa ttt gct aac acg cat gcg tat ttg aaa gag				1126
Gly Val Val Cys Glu Gln Phe Ala Asn Thr His Ala Tyr Leu Lys Glu	325	330	335	
tct aaa gaa atg gtg gta aaa gaa tgt ttt gaa gaa gaa gag cac ttt				1174
Ser Lys Glu Met Val Val Lys Glu Cys Phe Glu Glu Glu Glu His Phe	340	345	350	
tta gag act ttg gaa tgc ggc atg gaa ttg ttt aac ttg tct tta aag				1222
Leu Glu Thr Leu Glu Ser Gly Met Glu Leu Phe Asn Leu Ser Leu Lys	355	360	365	
cat ttg aat gaa aat aaa atc ttt gat ggc aag atc gct ttc aag ctt				1270
His Leu Asn Glu Asn Lys Ile Phe Asp Gly Lys Ile Ala Phe Lys Leu	370	375	380	385
tat gac act ttt ggt ttc cct ttg gat tta aca aac gac atg tta aga				1318
Tyr Asp Thr Phe Gly Phe Pro Leu Asp Leu Thr Asn Asp Met Leu Arg	390	395	400	
agt cat ggg gcg tgt gcg gat atg caa ggc ttt gaa ttg tgc atg caa				1366
Ser His Gly Ala Cys Ala Asp Met Gln Gly Phe Glu Leu Cys Met Gln	405	410	415	
gag caa gtg aaa cgc tct aaa gct tca tgg aaa ggc aaa caa aac aac				1414
Glu Gln Val Lys Arg Ser Lys Ala Ser Trp Lys Gly Lys Gln Asn Asn	420	425	430	
gcc gat ttt agc gct att tta aac gct tat gca cct aat gtt ttt gtg				1462
Ala Asp Phe Ser Ala Ile Leu Asn Ala Tyr Ala Pro Asn Val Phe Val	435	440	445	
ggg tat gaa acg aca gaa tgt tct gct aaa gtt tta ggg ttt ttt gat				1510
Gly Tyr Glu Thr Thr Glu Cys Ser Ala Lys Val Leu Gly Phe Phe Asp	450	455	460	465
agc gat ttt aaa gaa ata acc gat gca aat cct aac caa gaa gtc tgg				1558
Ser Asp Phe Lys Glu Ile Thr Asp Ala Asn Pro Asn Gln Glu Val Trp	470	475	480	
gtg ttg tta gaa aaa acc cct ttt tat gca gaa ggt gga ggg gct ata				1606
Val Leu Leu Glu Lys Thr Pro Phe Tyr Ala Glu Gly Gly Gly Ala Ile	485	490	495	
ggc gat agg ggc gcg ctt ttt aaa gac aat gga gaa gtg gct atc gtg				1654
Gly Asp Arg Gly Ala Leu Phe Lys Asp Asn Gly Glu Val Ala Ile Val	500	505	510	
tta gat aca aaa aac ttt ttt ggg ctt aat ttt tca ctc ctt gaa atc				1702
Leu Asp Thr Lys Asn Phe Phe Gly Leu Asn Phe Ser Leu Leu Glu Ile	515	520	525	
aaa aaa gcg cta aaa aaa ggc gat caa gtg atc gcg caa gtg agc gat				1750

Lys	Lys	Ala	Leu	Lys	Lys	Gly	Asp	Gln	Val	Ile	Ala	Gln	Val	Ser	Asp	
530					535					540					545	
gag	cgc	ttt	gaa	atc	gcc	aaa	cac	cat	agt	gcg	act	cat	tta	ttg	cag	1798
Glu	Arg	Phe	Glu	Ile	Ala	Lys	His	His	Ser	Ala	Thr	His	Leu	Leu	Gln	
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agc	gct	tta	aga	gaa	gtt	tta	ggc	tcg	cat	gtg	agt	caa	gcg	ggg	agt	1846
Ser	Ala	Leu	Arg	Glu	Val	Leu	Gly	Ser	His	Val	Ser	Gln	Ala	Gly	Ser	
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tta	gtg	gaa	tcc	aag	cga	ttg	cgc	ttt	gat	ttc	tcg	cat	gct	aaa	gcg	1894
Leu	Val	Glu	Ser	Lys	Arg	Leu	Arg	Phe	Asp	Phe	Ser	His	Ala	Lys	Ala	
		580					585					590				
ctc	aat	gat	gaa	gag	cta	gaa	aaa	gta	gaa	gat	tta	gtc	aac	gct	caa	1942
Leu	Asn	Asp	Glu	Glu	Leu	Glu	Lys	Val	Glu	Asp	Leu	Val	Asn	Ala	Gln	
	595					600					605					
att	ttc	aag	cac	cta	aat	agc	cag	gtg	gag	cat	atg	cct	tta	aac	caa	1990
Ile	Phe	Lys	His	Leu	Asn	Ser	Gln	Val	Glu	His	Met	Pro	Leu	Asn	Gln	
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gcc	aaa	gat	aag	gga	gcg	tta	gcg	tta	ttc	agt	gaa	aaa	tac	gct	gaa	2038
Ala	Lys	Asp	Lys	Gly	Ala	Leu	Ala	Leu	Phe	Ser	Glu	Lys	Tyr	Ala	Glu	
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aat	gtg	cgg	gtg	gtg	agc	ttt	aaa	gaa	gcg	tcc	att	gaa	ttg	tgt	ggg	2086
Asn	Val	Arg	Val	Val	Ser	Phe	Lys	Glu	Ala	Ser	Ile	Glu	Leu	Cys	Gly	
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ggc	att	cat	gtg	gaa	aat	act	ggg	ctt	att	ggg	ggg	ttt	agg	att	gta	2134
Gly	Ile	His	Val	Glu	Asn	Thr	Gly	Leu	Ile	Gly	Gly	Phe	Arg	Ile	Val	
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Lys	Glu	Ser	Gly	Val	Ser	Ser	Gly	Val	Arg	Arg	Ile	Glu	Ala	Val	Cys	
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ggg	aaa	gcc	ttt	tac	caa	ctg	gct	aaa	gaa	gaa	aat	aaa	gag	ctt	aaa	2230
Gly	Lys	Ala	Phe	Tyr	Gln	Leu	Ala	Lys	Glu	Glu	Asn	Lys	Glu	Leu	Lys	
	690				695				700						705	
aac	gct	aag	act	tta	ttg	aaa	aat	aac	gat	gtg	atc	gcc	ggt	atc	aat	2278
Asn	Ala	Lys	Thr	Leu	Leu	Lys	Asn	Asn	Asp	Val	Ile	Ala	Gly	Ile	Asn	
				710					715					720		
aag	ctt	aaa	gag	agc	gtg	aaa	aac	agc	caa	aaa	gcc	ccc	gtt	tct	atg	2326
Lys	Leu	Lys	Glu	Ser	Val	Lys	Asn	Ser	Gln	Lys	Ala	Pro	Val	Ser	Met	
			725					730					735			
gat	tta	ccg	gtt	gaa	aaa	atc	cat	ggc	gtg	aat	ttg	gtg	gtg	ggc	gta	2374
Asp	Leu	Pro	Val	Glu	Lys	Ile	His	Gly	Val	Asn	Leu	Val	Val	Gly	Val	
		740				745						750				
gtg	gaa	caa	ggc	gac	att	aaa	gaa	atg	att	gac	cga	ttg	aaa	agt	aag	2422
Val	Glu	Gln	Gly	Asp	Ile	Lys	Glu	Met	Ile	Asp	Arg	Leu	Lys	Ser	Lys	
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cat gaa aga ttg ctc gct atg gtg ttt aaa aaa gaa aat gag cga atc	2470
His Glu Arg Leu Leu Ala Met Val Phe Lys Lys Glu Asn Glu Arg Ile	
770 775 780 785	
act ctc gca tgc ggg gtg aaa aac gcg ccc ata aaa gcg aat gtg tgg	2518
Thr Leu Ala Cys Gly Val Lys Asn Ala Pro Ile Lys Ala Asn Val Trp	
790 795 800	
gct aat gaa gtg gcg caa att tta ggg ggc aaa ggg ggc ggg aga ggt	2566
Ala Asn Glu Val Ala Gln Ile Leu Gly Gly Lys Gly Gly Arg Gly	
805 810 815	
gat ttt gcg agc gct gga ggc aag gat att gaa aat ttg caa gcc gca	2614
Asp Phe Ala Ser Ala Gly Gly Lys Asp Ile Glu Asn Leu Gln Ala Ala	
820 825 830	
ctc aat tta gcg aaa aat acc gct ctt aaa gct tta gag gga	2656
Leu Asn Leu Ala Lys Asn Thr Ala Leu Lys Ala Leu Glu Gly	
835 840 845	
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Phe Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile	
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Val Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met	
50 55 60	
Arg Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly Tyr Thr Ala	
65 70 75 80	
Arg His His Thr Leu Phe Glu Met Leu Gly Asn Phe Ser Phe Gly Asp	
85 90 95	
Tyr Phe Lys Glu Glu Ala Ile Leu Phe Ala Trp Glu Phe Val Thr Lys	
100 105 110	
Asn Leu Gly Phe Lys Pro Lys Asp Leu Tyr Ile Ser Val His Glu Lys	
115 120 125	
Asp Asp Glu Ala Val Lys Leu Trp Glu Lys Phe Val Pro Val Asp Arg	
130 135 140	
Ile Lys Lys Met Gly Asp Lys Asp Asn Phe Trp Gln Met Gly Asp Ser	
145 150 155 160	
Gly Pro Cys Gly Pro Cys Ser Glu Ile Tyr Ile Asp Gln Gly Glu Lys	
165 170 175	
His Phe Lys Gly Ser Glu Asp Tyr Phe Gly Gly Glu Gly Asp Arg Phe	
180 185 190	
Leu Glu Ile Trp Asn Leu Val Phe Met Gln Tyr Glu Arg Ser Asn Asp	
195 200 205	
Gly Val Leu Ser Pro Leu Pro Lys Pro Ser Ile Asp Thr Gly Met Gly	
210 215 220	
Leu Glu Arg Val Gln Ala Leu Leu Glu His Lys Leu Asn Asn Phe Asp	

225					230					235				240
Ser	Ser	Leu	Phe	Ala	Pro	Leu	Met	Glu	Glu	Ile	Ser	Glu	Leu	Thr
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Leu	Asp	Tyr	Ala	Ser	Glu	Phe	Gln	Pro	Ser	Phe	Arg	Val	Val	Ala
			260					265					270	Asp
His	Ala	Arg	Ala	Val	Ala	Phe	Leu	Leu	Ala	Gln	Gly	Val	His	Phe
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Lys	Glu	Gly	Arg	Gly	Tyr	Val	Leu	Arg	Arg	Ile	Leu	Arg	Arg	Ala
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Arg	His	Gly	Tyr	Leu	Met	Gly	Leu	Lys	Glu	Ala	Phe	Leu	Tyr	Lys
305					310					315				Val
Val	Gly	Val	Val	Cys	Glu	Gln	Phe	Ala	Asn	Thr	His	Ala	Tyr	Leu
				325					330					Lys
Glu	Ser	Lys	Glu	Met	Val	Val	Lys	Glu	Cys	Phe	Glu	Glu	Glu	Glu
			340					345					350	His
Phe	Leu	Glu	Thr	Leu	Glu	Ser	Gly	Met	Glu	Leu	Phe	Asn	Leu	Ser
			355				360					365		Leu
Lys	His	Leu	Asn	Glu	Asn	Lys	Ile	Phe	Asp	Gly	Lys	Ile	Ala	Phe
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Leu	Tyr	Asp	Thr	Phe	Gly	Phe	Pro	Leu	Asp	Leu	Thr	Asn	Asp	Met
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Arg	Ser	His	Gly	Ala	Cys	Ala	Asp	Met	Gln	Gly	Phe	Glu	Leu	Cys
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Gln	Glu	Gln	Val	Lys	Arg	Ser	Lys	Ala	Ser	Trp	Lys	Gly	Lys	Gln
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Asn	Ala	Asp	Phe	Ser	Ala	Ile	Leu	Asn	Ala	Tyr	Ala	Pro	Asn	Val
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Val	Gly	Tyr	Glu	Thr	Thr	Glu	Cys	Ser	Ala	Lys	Val	Leu	Gly	Phe
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Asp	Ser	Asp	Phe	Lys	Glu	Ile	Thr	Asp	Ala	Asn	Pro	Asn	Gln	Glu
465					470					475				Val
Trp	Val	Leu	Leu	Glu	Lys	Thr	Pro	Phe	Tyr	Ala	Glu	Gly	Gly	Gly
				485					490					Ala
Ile	Gly	Asp	Arg	Gly	Ala	Leu	Phe	Lys	Asp	Asn	Gly	Glu	Val	Ile
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Val	Leu	Asp	Thr	Lys	Asn	Phe	Phe	Gly	Leu	Asn	Phe	Ser	Leu	Leu
			515				520					525		Glu
Ile	Lys	Lys	Ala	Leu	Lys	Lys	Gly	Asp	Gln	Val	Ile	Ala	Gln	Val
530						535					540			Ser
Asp	Glu	Arg	Phe	Glu	Ile	Ala	Lys	His	His	Ser	Ala	Thr	His	Leu
545					550					555				Leu
Gln	Ser	Ala	Leu	Arg	Glu	Val	Leu	Gly	Ser	His	Val	Ser	Gln	Ala
				565					570					Gly
Ser	Leu	Val	Glu	Ser	Lys	Arg	Leu	Arg	Phe	Asp	Phe	Ser	His	Lys
			580					585					590	
Ala	Leu	Asn	Asp	Glu	Glu	Leu	Glu	Lys	Val	Glu	Asp	Leu	Val	Asn
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Gln	Ile	Phe	Lys	His	Leu	Asn	Ser	Gln	Val	Glu	His	Met	Pro	Leu
610						615					620			Asn
Gln	Ala	Lys	Asp	Lys	Gly	Ala	Leu	Ala	Leu	Phe	Ser	Glu	Lys	Tyr
625					630					635				Ala
Glu	Asn	Val	Arg	Val	Val	Ser	Phe	Lys	Glu	Ala	Ser	Ile	Glu	Leu
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Gly	Gly	Ile	His	Val	Glu	Asn	Thr	Gly	Leu	Ile	Gly	Gly	Phe	Arg
			660					665					670	Ile
Val	Lys	Glu	Ser	Gly	Val	Ser	Ser	Gly	Val	Arg	Arg	Ile	Glu	Ala
			675				680					685		Val
Cys	Gly	Lys	Ala	Phe	Tyr	Gln	Leu	Ala	Lys	Glu	Glu	Asn	Lys	Glu
690						695					700			Leu

Leu	Gln	Phe	Met	Asp	Lys	Lys	Ser	Asp	Asn	Pro	Gln	Ala	Asn	Ala	Met		
			105					110					115				
caa	gat	agt	ata	atg	cat	gag	aat	tcc	aac	aac	gct	tat	ccc	gct	aat		498
Gln	Asp	Ser	Ile	Met	His	Glu	Asn	Ser	Asn	Asn	Ala	Tyr	Pro	Ala	Asn		
		120					125					130					
cat	aac	gct	ccc	agc	caa	gat	cct	ttt	aac	caa	gct	tat	gcg	caa	aac		546
His	Asn	Ala	Pro	Ser	Gln	Asp	Pro	Phe	Asn	Gln	Ala	Tyr	Ala	Gln	Asn		
	135					140					145						
gct	tac	gct	aaa	gag	aat	tta	caa	gca	cag	ccg	tcc	aag	tat	caa	aac		594
Ala	Tyr	Ala	Lys	Glu	Asn	Leu	Gln	Ala	Gln	Pro	Ser	Lys	Tyr	Gln	Asn		
150					155					160					165		
agc	gtg	cct	gaa	atc	aat	att	gat	gaa	gaa	gaa	atc	ccc	ttt				636
Ser	Val	Pro	Glu	Ile	Asn	Ile	Asp	Glu	Glu	Glu	Ile	Pro	Phe				
				170						175							
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			20					25					30				
Thr	Ser	Arg	Arg	Phe	Lys	Lys	Gln	Asp	Gly	Thr	Leu	Gly	Glu	Glu	Val		
		35					40					45					
Cys	Phe	Ile	Asp	Ala	Arg	Leu	Phe	Gly	Arg	Thr	Ala	Glu	Ile	Ala	Asn		
	50					55				60							
Gln	Tyr	Leu	Ser	Lys	Gly	Ser	Ser	Val	Leu	Ile	Glu	Gly	Arg	Leu	Thr		
65					70					75					80		
Tyr	Glu	Ser	Trp	Met	Asp	Gln	Thr	Gly	Lys	Lys	Asn	Ser	Arg	His	Thr		
			85					90						95			
Ile	Thr	Ala	Asp	Ser	Leu	Gln	Phe	Met	Asp	Lys	Lys	Ser	Asp	Asn	Pro		
			100					105					110				
Gln	Ala	Asn	Ala	Met	Gln	Asp	Ser	Ile	Met	His	Glu	Asn	Ser	Asn	Asn		
		115				120						125					
Ala	Tyr	Pro	Ala	Asn	His	Asn	Ala	Pro	Ser	Gln	Asp	Pro	Phe	Asn	Gln		
	130					135					140						
Ala	Tyr	Ala	Gln	Asn	Ala	Tyr	Ala	Lys	Glu	Asn	Leu	Gln	Ala	Gln	Pro		
145				150						155					160		
Ser	Lys	Tyr	Gln	Asn	Ser	Val	Pro	Glu	Ile	Asn	Ile	Asp	Glu	Glu	Glu		
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Met Lys Leu Lys Ser Phe Gly Val	
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ttt gga aat ccc att aag cat tcc aaa tcg ccc tta atc cat aac gct	162
Phe Gly Asn Pro Ile Lys His Ser Lys Ser Pro Leu Ile His Asn Ala	
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tgt ttt tta act ttt caa aaa gaa tta agg ttt ttg ggg cat tac cac	210
Cys Phe Leu Thr Phe Gln Lys Glu Leu Arg Phe Leu Gly His Tyr His	
25 30 35 40	
ccc ata tta ctc cct tta gaa agc cac atc aaa agc gag ttt ttg cat	258
Pro Ile Leu Leu Pro Leu Glu Ser His Ile Lys Ser Glu Phe Leu His	
45 50 55	
ttg gga ttg agt ggg gct aat gta acc tta ccc ttt aaa gaa agg gcg	306
Leu Gly Leu Ser Gly Ala Asn Val Thr Leu Pro Phe Lys Glu Arg Ala	
60 65 70	
ttt caa gtt tgc gat aaa atc aaa ggt atc gcg ctt gaa tgc gga gcg	354
Phe Gln Val Cys Asp Lys Ile Lys Gly Ile Ala Leu Glu Cys Gly Ala	
75 80 85	
gtc aat acg ctt gtt tta gaa aat gat gag ctt gtg ggt tac aat acc	402
Val Asn Thr Leu Val Leu Glu Asn Asp Glu Leu Val Gly Tyr Asn Thr	
90 95 100	
gac gct tta ggg ttt tat ctt tct tta aag caa aaa aac tat caa aac	450
Asp Ala Leu Gly Phe Tyr Leu Ser Leu Lys Gln Lys Asn Tyr Gln Asn	
105 110 115 120	
gct ttg att tta gga gct ggg ggg agc gct aaa gcc cta gcg tgt gaa	498
Ala Leu Ile Leu Gly Ala Gly Gly Ser Ala Lys Ala Leu Ala Cys Glu	
125 130 135	
ttg aaa aaa caa ggc tta caa gtg agc gtg ttg aac cgc tct tct agg	546
Leu Lys Lys Gln Gly Leu Gln Val Ser Val Leu Asn Arg Ser Ser Arg	
140 145 150	
gga ttg gat ttt ttc caa cgc ctg ggc tgt gat tgt ttt atg gag cct	594
Gly Leu Asp Phe Phe Gln Arg Leu Gly Cys Asp Cys Phe Met Glu Pro	
155 160 165	
cct aaa agc gct ttt gat ttg att att aac gcc act tca gcg agt ttg	642
Pro Lys Ser Ala Phe Asp Leu Ile Ile Asn Ala Thr Ser Ala Ser Leu	
170 175 180	
cat aac gaa ttg cct ttg aat aaa gag gtt ttg aaa ggg tat ttt aaa	690
His Asn Glu Leu Pro Leu Asn Lys Glu Val Leu Lys Gly Tyr Phe Lys	
185 190 195 200	
gag ggc aag ctc gct tat gat ttg gcg tat ggg ttt tta acg ccc ttt	738
Glu Gly Lys Leu Ala Tyr Asp Leu Ala Tyr Gly Phe Leu Thr Pro Phe	

205	210	215	
ttg tct tta gcc aaa gag tta aaa acc cct ttt caa gac gga aaa gac			786
Leu Ser Leu Ala Lys Glu Leu Lys Thr Pro Phe Gln Asp Gly Lys Asp			
220	225	230	
atg ctc atc tat caa gct gct tta agt ttt gaa aaa ttc agc gct tct			834
Met Leu Ile Tyr Gln Ala Ala Leu Ser Phe Glu Lys Phe Ser Ala Ser			
235	240	245	
caa atc cct tat tca aaa gcg ttt gaa gtc atg cga agt gtt ttt			879
Gln Ile Pro Tyr Ser Lys Ala Phe Glu Val Met Arg Ser Val Phe			
250	255	260	
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Gly	Cys	Asp	Cys	Phe	Met	Glu	Pro	Pro	Lys	Ser	Ala	Phe	Asp	Leu	Ile
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Ile	Asn	Ala	Thr	Ser	Ala	Ser	Leu	His	Asn	Glu	Leu	Pro	Leu	Asn	Lys
			180					185					190		
Glu	Val	Leu	Lys	Gly	Tyr	Phe	Lys	Glu	Gly	Lys	Leu	Ala	Tyr	Asp	Leu
		195					200					205			
Ala	Tyr	Gly	Phe	Leu	Thr	Pro	Phe	Leu	Ser	Leu	Ala	Lys	Glu	Leu	Lys
		210				215					220				
Thr	Pro	Phe	Gln	Asp	Gly	Lys	Asp	Met	Leu	Ile	Tyr	Gln	Ala	Ala	Leu
225					230					235				240	
Ser	Phe	Glu	Lys	Phe	Ser	Ala	Ser	Gln	Ile	Pro	Tyr	Ser	Lys	Ala	Phe
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Glu	Val	Met	Arg	Ser	Val	Phe									
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<211> 1080
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Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val Ala Val Phe	
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Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys Val Leu Ala	
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Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro Phe Gly Leu	
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Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys Glu Asp Ile	
55 60 65	
atc cct caa ggc gcg aac aaa ttc att ttc acg cta gcg ccc att att	295
Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala Pro Ile Ile	
70 75 80	
gcg atg gtg agt gcg ttt gtg tcc atg gcg cct atc ccc ttt ttc cct	343
Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro Phe Phe Pro	
85 90 95	
aat ttc act ctg ttt ggc tat gag atc aag ccc ctt att tct gac atc	391
Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile Ser Asp Ile	
100 105 110 115	
aac att ggc ttt ttg ttt ttc tta gcc gtg ggt tcg gca ggg att tat	439
Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala Gly Ile Tyr	
120 125 130	
gcg cct att tta gcc ggg ctt gcc tct aat aac aaa tac tct tta att	487
Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser Leu Ile	
135 140 145	
ggc tcc gca aga gcg acg atc caa ctg ctc agc ttt gaa gtg gtc agc	535
Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val Val Ser	
150 155 160	
act tta acc att cta gcc ccc tta atg gtg gta gga tcg ctc tct tta	583
Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu Ser Leu	
165 170 175	
gtg gaa atc aat cat tac caa agc ggt ggg ttt tta gac tgg ctt gtg	631
Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp Leu Val	

180	185	190	195	
ttt aag cag cct cta gcg ttt gtt ttg ttt ttg atc gca agt tat gcc				679
Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala Ser Tyr Ala				
200		205	210	
gaa ttg aat cga acc ccc ttt gac ttg cta gag cat gaa gcc gag atc				727
Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu Ala Glu Ile				
215		220	225	
gtg gcg ggg tat tgc acc gaa tac agc ggc ttg aaa tgg ggc atg ttc				775
Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp Gly Met Phe				
230		235	240	
ttt tta gcg gaa tac gcg cat tta ttc gct ttt tct ttt gtg att tct				823
Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe Val Ile Ser				
245		250	255	
att gtg ttt ttt ggc ggg ttt aac gca tgg ggc ttt atc cct gga ggc				871
Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile Pro Gly Gly				
260		265	270	275
ata gcg att ttg att aaa gcg ggc ttt ttt gtc ttt tta tcc atg tgg				919
Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu Ser Met Trp				
280		285	290	
gtt aga gcg act tat ccg cat gtg cgc cca gac caa ctg atg gat atg				967
Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu Met Asp Met				
295		300	305	
tgc tgg aaa atc atg ctg cct tta gcg tta ttg aac att gtg cta acg				1015
Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile Val Leu Thr				
310		315	320	
ggc att atc att tta att taaaggaggt tttatggcca aacaagaata				1063
Gly Ile Ile Ile Leu Ile				
325				
caagcaactt cctaaac				1080
<210> 170				
<211> 329				
<212> PRT				
<213> Helicobacter pylori				
<400> 170				
Met Ser Ala Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val				
1 5 10 15				
Ala Val Phe Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys				
20 25 30				
Val Leu Ala Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro				
35 40 45				
Phe Gly Leu Leu Gln Val Ala Asp Gly Ile Lys Leu Phe Thr Lys				
50 55 60				
Glu Asp Ile Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala				
65 70 75 80				
Pro Ile Ile Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro				
85 90 95				
Phe Phe Pro Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile				

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          100          105          110
Ser Asp Ile Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala
          115          120          125
Gly Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr
          130          135          140
Ser Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu
145          150          155          160
Val Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser
          165          170          175
Leu Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp
          180          185          190
Trp Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala
          195          200          205
Ser Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu
          210          215          220
Ala Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp
225          230          235          240
Gly Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe
          245          250          255
Val Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile
          260          265          270
Pro Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu
          275          280          285
Ser Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu
          290          295          300
Met Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile
305          310          315          320
Val Leu Thr Gly Ile Ile Ile Leu Ile
          325

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<210> 171
 <211> 1280
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (48)...(1226)

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          <400> 171
taaggataaa atcaagcgat tagcccgaat ttttaagagag tattaag atg aat aaa      56
                                     Met Asn Lys
                                     1

aaa gcg tat ttt ggg gag ttt gga ggg agt ttt gtt tcg gag ttg tta      104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu
          5          10          15

gtg cct gca tta aga gaa tta gaa cag gcg ttt gat gcg tgt ttg aaa      152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys
          20          25          30          35

gat gaa aaa ttc caa aaa gaa tat ttt cgt ctt tta aag gat ttt gtg      200
Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val
          40          45          50

ggc cgt cct agc cct tta acc ttg tgt caa aat atc gtt tct aac cct      248
Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro
          55          60          65

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aaa gtc aag ctt tat tta aaa cga gag gat tta atc cat ggc ggg gcg Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His Gly Gly Ala 70 75 80	296
cat aag act aat caa gcc tta ggg caa gcc ctt tta gcg aaa aaa atg His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala Lys Lys Met 85 90 95	344
ggt aaa aca agg atc atc gct gaa aca ggc gcc ggt cag cat ggc gtg Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Val 100 105 110 115	392
gcg acg gct atc gct tgc gca tta ttg aac tta aaa tgc gtg gtt ttt Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys Val Val Phe 120 125 130	440
atg gga tct aaa gac atc aag cgc cag gaa atg aat gtt ttt aga atg Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val Phe Arg Met 135 140 145	488
cac tta tta ggc gct gaa gtg aga gag gtt aat tca ggg agc gcg acg His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly Ser Ala Thr 150 155 160	536
ctt aaa gac gct gtg aat gaa gcc tta aga gat tgg gcg agc agt tac Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala Ser Ser Tyr 165 170 175	584
aag gac acg cat tat ttg cta ggc aca gcc gcc ggg cca cac cct tac Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro His Pro Tyr 180 185 190 195	632
ccc aca atg gtt aaa acc ttt caa aaa atg ata ggc gat gag gtt aaa Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp Glu Val Lys 200 205 210	680
agc cag att tta gaa aaa gaa aac cgc ttg cct gat tat gtg atc gca Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr Val Ile Ala 215 220 225	728
tgc gtt gga ggg ggg tct aac gct ata ggg ata ttc agc gca ttt tta Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser Ala Phe Leu 230 235 240	776
aac gac aaa gaa gtt aaa ctc ata ggc gta gag ccg gcg ggt tta ggg Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala Gly Leu Gly 245 250 255	824
cta gaa acc aat aag cat ggg gcg act ttg aat aag ggg cgt gtg ggg Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly Arg Val Gly 260 265 270 275	872
att ttg cat ggg aat aaa acc tat ctt tta caa gat gat gaa ggc cag Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln 280 285 290	920
att gca gaa agc cat agc att agc gcc ggg ctt gat tat cca gga gtg Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val	968

[illegible]

195 200 205
 Glu Val Lys Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr
 210 215 220
 Val Ile Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser
 225 230 235 240
 Ala Phe Leu Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala
 245 250 255
 Gly Leu Gly Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly
 260 265 270
 Arg Val Gly Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp
 275 280 285
 Glu Gly Gln Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr
 290 295 300
 Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala
 305 310 315 320
 Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu
 325 330 335
 Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala
 340 345 350
 Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Ser Ile
 355 360 365
 Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val
 370 375 380
 Tyr Asn Ala Leu Lys Gly Gly Leu Lys
 385 390

<210> 173
 <211> 559
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (31)...(513)

<400> 173
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 Met Asn Val Lys Asn Arg Leu Ser
 1 5
 gat tgg gaa tat caa tgg gca gtg gct cta gtc tat acg ata tgt atc 102
 Asp Trp Glu Tyr Gln Trp Ala Val Ala Leu Val Tyr Thr Ile Cys Ile
 10 15 20
 tcc ata aac gct agg att ttt tat gac ata gat ggt tca gct agc gat 150
 Ser Ile Asn Ala Arg Ile Phe Tyr Asp Ile Asp Gly Ser Ala Ser Asp
 25 30 35 40
 tcg att ttt gac cct aaa aat agc tat tat atg tgg cta gtg ggt cta 198
 Ser Ile Phe Asp Pro Lys Asn Ser Tyr Tyr Met Trp Leu Val Gly Leu
 45 50 55
 ata gcg gct ttg ttg tct aac ctt tta ttt gac cca cga ggt agg gat 246
 Ile Ala Ala Leu Leu Ser Asn Leu Leu Phe Asp Pro Arg Gly Arg Asp
 60 65 70
 tgt tat aaa tct ttc caa gta aga tac cct agg ttt ctc aaa gcc att 294
 Cys Tyr Lys Ser Phe Gln Val Arg Tyr Pro Arg Phe Leu Lys Ala Ile
 75 80 85

<222> (53)...(712)

<400> 175

tgagatcaaa cccgtagaac ttgtcaaggt aattcttgcg taaggaaata gc atg tta	58
Met Leu	
1	
ata acc acc caa cta tcc aaa cga ttt tac gcc aca ctc gct ctt tct	106
Ile Thr Thr Gln Leu Ser Lys Arg Phe Tyr Ala Thr Leu Ala Leu Ser	
5 10 15	
tgc gtg ttt tta acc atc act aac att ctt gtc aaa ggc tcg ttt atc	154
Cys Val Phe Leu Thr Ile Thr Asn Ile Leu Val Lys Gly Ser Phe Ile	
20 25 30	
aat ctt tta gca ggg ctt agt ggg gtt ttg tat gcg ttt ttt gcc gga	202
Asn Leu Leu Ala Gly Leu Ser Gly Val Leu Tyr Ala Phe Phe Ala Gly	
35 40 45 50	
gaa agg caa acg att tgc ttt gtg ttt ggt ctt gtt tat aat ttg agt	250
Glu Arg Gln Thr Ile Cys Phe Val Phe Gly Leu Val Tyr Asn Leu Ser	
55 60 65	
tac gct tat gtc gct tat cag tgg aaa tta aac gct gat gtg att tta	298
Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val Ile Leu	
70 75 80	
tgc ctt ttt ttg tat atg cca gta acg att tat ggg ctg ttc gca tgg	346
Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe Ala Trp	
85 90 95	
aaa aag aca gag cag cat gaa ggc gtt atc aag gct caa aaa ctt tcc	394
Lys Lys Thr Glu Gln His Glu Gly Val Ile Lys Ala Gln Lys Leu Ser	
100 105 110	
aaa aat tgg cgt ttt ata ctc att tta ggc gta ggg gtt tta act tgt	442
Lys Asn Trp Arg Phe Ile Leu Ile Leu Gly Val Gly Val Leu Thr Cys	
115 120 125 130	
gtg agc gct ttg ttt ttt aaa gag att aaa acg aat ttt tta tgg gca	490
Val Ser Ala Leu Phe Phe Lys Glu Ile Lys Thr Asn Phe Leu Trp Ala	
135 140 145	
gag agt ttt aat ttc gtc atc ttt att att gct ttt att tta cag gtt	538
Glu Ser Phe Asn Phe Val Ile Phe Ile Ile Ala Phe Ile Leu Gln Val	
150 155 160	
ttg cgc tat ata gaa aat tat gcg cta gta act ttg ggg aat atc gta	586
Leu Arg Tyr Ile Glu Asn Tyr Ala Leu Val Thr Leu Gly Asn Ile Val	
165 170 175	
tcc att atc gtg tgg ttt tgt att ttt caa att tct aca gag agc ttg	634
Ser Ile Ile Val Trp Phe Cys Ile Phe Gln Ile Ser Thr Glu Ser Leu	
180 185 190	
gtg caa ctc ttc aca acg atc cta tac ctt ttt att ggc ttg tat tat	682
Val Gln Leu Phe Thr Thr Ile Leu Tyr Leu Phe Ile Gly Leu Tyr Tyr	
195 200 205 210	

<220>
 <221> CDS
 <222> (36)...(1142)

<400> 179

aaaataagcg ttttgatgcc atttttggag cgatc	gtg gaa ttg agt tat tat	53
	Val Glu Leu Ser Tyr Tyr	
	1 5	
gaa att tta gaa gtg gaa aaa cac agc aac caa gag acc att aaa aag	101	
Glu Ile Leu Glu Val Glu Lys His Ser Asn Gln Glu Thr Ile Lys Lys		
10 15 20		
tct tac aga aag ctg gct tta aaa tac cac cca gac aga aac gcc ggc	149	
Ser Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro Asp Arg Asn Ala Gly		
25 30 35		
gat aaa gaa gcc gaa gaa aaa ttc aag ctc atc aat gaa gcc tat ggg	197	
Asp Lys Glu Ala Glu Glu Lys Phe Lys Leu Ile Asn Glu Ala Tyr Gly		
40 45 50		
gtg tta agc gat gaa aag aag cgg gcc tta tac gac agg tat ggt aaa	245	
Val Leu Ser Asp Glu Lys Lys Arg Ala Leu Tyr Asp Arg Tyr Gly Lys		
55 60 65 70		
aaa ggc tta aac caa gcc ggc gca agc caa ggc gat ttt tct gat ttt	293	
Lys Gly Leu Asn Gln Ala Gly Ala Ser Gln Gly Asp Phe Ser Asp Phe		
75 80 85		
ttt gaa gat tta ggc tcg ttt ttt gaa gac gct ttt ggg ttt ggc gct	341	
Phe Glu Asp Leu Gly Ser Phe Phe Glu Asp Ala Phe Gly Phe Gly Ala		
90 95 100		
agg ggg agt aaa agg caa aaa agc tct atc gca ccg gat tat ttg caa	389	
Arg Gly Ser Lys Arg Gln Lys Ser Ser Ile Ala Pro Asp Tyr Leu Gln		
105 110 115		
acc ctt gaa ttg agt ttc aaa gaa gcg gtt ttt ggc tgt aaa aaa acc	437	
Thr Leu Glu Leu Ser Phe Lys Glu Ala Val Phe Gly Cys Lys Lys Thr		
120 125 130		
att aaa gtc caa tac cag agc gtt tgt gaa agt tgc gat ggc acg ggc	485	
Ile Lys Val Gln Tyr Gln Ser Val Cys Glu Ser Cys Asp Gly Thr Gly		
135 140 145 150		
gct aaa gac aaa gcc cta gag act tgc aag caa tgc aat ggg cag ggc	533	
Ala Lys Asp Lys Ala Leu Glu Thr Cys Lys Gln Cys Asn Gly Gln Gly		
155 160 165		
cag gtg ttt atg cgt caa ggt ttt atg agt ttt gcg caa act tgt ggc	581	
Gln Val Phe Met Arg Gln Gly Phe Met Ser Phe Ala Gln Thr Cys Gly		
170 175 180		
gcg tgt caa ggc aag ggc aag atc gtt aaa acc cca tgc caa gcg tgc	629	
Ala Cys Gln Gly Lys Gly Lys Ile Val Lys Thr Pro Cys Gln Ala Cys		
185 190 195		
aag ggt aaa acc tat atc ctt aaa gat gaa gaa att gat gcg ata atc	677	
Lys Gly Lys Thr Tyr Ile Leu Lys Asp Glu Glu Ile Asp Ala Ile Ile		

200	205	210	
cct gag ggc att gat gat Pro Glu Gly Ile Asp Asp 215 220	caa aac cgc atg gtg Gln Asn Arg Met Val 225	ctt aaa aat aaa ggc Leu Lys Asn Lys Gly 230	725
aat gaa tac gag aag gga Asn Glu Tyr Glu Lys Gly 235	aaa aga ggg gat ttg Lys Arg Gly Asp Leu 240	tat tta gaa gcg caa Tyr Leu Glu Ala Gln 245	773
gtc aaa gaa gat gag cat Val Lys Glu Asp Glu His 250	ttc aag cgc gaa ggc Phe Lys Arg Glu Gly 255	tgc gat tta ttc att Cys Asp Leu Phe Ile 260	821
aaa gcg ccg gtg ttt ttc Lys Ala Pro Val Phe Phe 265	acc act atc gct tta Thr Thr Ile Ala Leu 270	ggg cat acg att aaa Gly His Thr Ile Lys 275	869
gtg ccg tct tta aaa ggg Val Pro Ser Leu Lys Gly 280	gac gaa ctg gaa tta Asp Glu Leu Glu Leu 285	aaa atc cct aga aac Lys Ile Pro Arg Asn 290	917
gcc aga gac aag cag act Ala Arg Asp Lys Gln Thr 295 300	ttt gcg ttt aga aac Phe Ala Phe Arg Asn 305	gag ggc gtg aaa cac Glu Gly Val Lys His 310	965
cct gaa agc tct tat aga Pro Glu Ser Ser Tyr Arg 315	ggg agt ttg atc gtg Gly Ser Leu Ile Val 320	gaa ttg caa gtg att Glu Leu Gln Val Ile 325	1013
tac cct aaa agt ttg aat Tyr Pro Lys Ser Leu Asn 330	aaa gag cag caa gaa Lys Glu Gln Gln Glu 335	ttg ttg gaa aaa ttg Leu Leu Glu Lys Leu 340	1061
cat gcg agt ttt ggc tat His Ala Ser Phe Gly Tyr 345	gag ggc gag ccg cat Glu Gly Glu Pro His 350	aaa agc gtt tta gaa Lys Ser Val Leu Glu 355	1109
acc tgt att tct aaa att Thr Cys Ile Ser Lys Ile 360	aaa gac tgg ttc aaa Lys Asp Trp Phe Lys 365	taaaagggttg ttgatgcatg	1162
agttttctaaa agcttttataa gacgctttcc ctcataccat tt			1204

<210> 180

<211> 369

<212> PRT

<213> Helicobacter pylori

<400> 180

Val	Glu	Leu	Ser	Tyr	Tyr	Glu	Ile	Leu	Glu	Val	Glu	Lys	His	Ser	Asn
1				5					10					15	
Gln	Glu	Thr	Ile	Lys	Lys	Ser	Tyr	Arg	Lys	Leu	Ala	Leu	Lys	Tyr	His
			20					25					30		
Pro	Asp	Arg	Asn	Ala	Gly	Asp	Lys	Glu	Ala	Glu	Glu	Lys	Phe	Lys	Leu
			35				40					45			
Ile	Asn	Glu	Ala	Tyr	Gly	Val	Leu	Ser	Asp	Glu	Lys	Lys	Arg	Ala	Leu
	50					55					60				
Tyr	Asp	Arg	Tyr	Gly	Lys	Lys	Gly	Leu	Asn	Gln	Ala	Gly	Ala	Ser	Gln

[illegible]

<210> 182
 <211> 256
 <212> PRT
 <213> Helicobacter pylori

<400> 182
 Met Arg Val Met Ala Lys Ile Glu Leu Leu Ala Lys Phe Thr Gln Ile
 1 5 10 15
 Ala Leu Pro Asn Ser His Pro Leu Leu Lys Lys Val Leu Asn Tyr Ala
 20 25 30
 Lys Lys His Phe Ser Gln Cys His Met Leu Ser Ser Ser Leu Leu Ile
 35 40 45
 Leu Asn Asp Thr Glu Cys Phe Lys Lys Asn Tyr Leu Leu Asn Trp Val
 50 55 60
 Tyr His Ala Leu Glu Cys Val His Glu Lys Asp Ile Ser Ala His Ser
 65 70 75 80
 Leu Glu Glu Val Leu Gln Lys Ser His Leu Pro Ile Arg Ile Lys Ile
 85 90 95
 Met Ala Gln Asn Thr Leu Leu Glu Lys Ile Glu Val Lys Val Leu Thr
 100 105 110
 Phe Gly Ala Glu Tyr Ala Leu Phe Ile Thr Lys His Pro Ile Ala Lys
 115 120 125
 Arg Phe Leu Arg Gln Lys Phe Ser Gly Cys Val Phe Leu Glu Thr Gln
 130 135 140
 Asp Glu Leu His Ile Arg Gly Asp Ser Glu Arg Phe Trp Glu Leu Ile
 145 150 155 160
 Val Thr Leu Asn Glu Asn Arg Ile Val His Asn Ala Cys Leu Asp Phe
 165 170 175
 Ile Tyr Pro Asn Gly Phe Gly Lys Asp Ser Tyr Thr Thr Met Ala Glu
 180 185 190
 Arg Lys Leu Lys Glu Cys Tyr Lys Thr Leu Gly Phe Ile Lys His Glu
 195 200 205
 Asp Phe Ser Glu Val Lys Lys Arg Tyr Leu Glu Leu Ala Lys Thr Tyr
 210 215 220
 His Pro Asp Leu Cys Asp Leu Lys Glu Lys Lys Ala Leu Tyr Ala Lys
 225 230 235 240
 Arg Phe Ala Ile Ile Gln Glu Ala Tyr Arg His Ile Lys Lys His Ala
 245 250 255

<210> 183
 <211> 900
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (59)...(778)

<400> 183
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 atg aag tca aat aaa aag tcc aat cgt tta aga gcg att tat aga gct 106
 Met Lys Ser Asn Lys Lys Ser Asn Arg Leu Arg Ala Ile Tyr Arg Ala
 1 5 10 15
 tta gtg atc gct ata gga cta gct gtt atc atc gtt ttc aat tac ttt 154
 Leu Val Ile Ala Ile Gly Leu Ala Val Ile Ile Val Phe Asn Tyr Phe
 20 25 30
 aac cgc aaa aac aat aac gcc cgc tcc agc cgt agg gct tgt tcg tgc 202

[illegible]

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<210> 184
<211> 240
<212> PRT
<213> Helicobacter pylori
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Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile Lys Asp Lys Glu Arg	
55 60 65	
ttc aag cct aaa gac gct tta atg gaa att agg ggg gat ttt agc atg	294
Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg Gly Asp Phe Ser Met	
70 75 80 85	
ctt tta aag gtt gag cgc acc ctt tta aac ctt ttg caa cac agc agc	342
Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu Leu Gln His Ser Ser	
90 95 100	
ggg att gct act tta acg agc cgt ttt gta gag gct tta aat tct cat	390
Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu Ala Leu Asn Ser His	
105 110 115	
aaa gtg cgt ttg ttg gac acg aga aaa acg aga ccc ctt tta agg atc	438
Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg Pro Leu Leu Arg Ile	
120 125 130	
ttt gaa aaa tat tcc gtg ctt aat ggg gga gcg agc aac cac cgc tta	486
Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala Ser Asn His Arg Leu	
135 140 145	
ggg cta gat gac gct tta atg ctt aaa gac acg cat tta agg cat gtg	534
Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr His Leu Arg His Val	
150 155 160 165	
aaa gat ctc aaa agc ttt tta acg cat gcc aga aaa aac ttg cct ttc	582
Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe	
170 175 180	
acg gct aaa att gaa att gaa tgc gaa agc ttt gaa gag gcc aaa aac	630
Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn	
185 190 195	
gcc atg aat gcg gga gcg gat att gtg atg tgc gat aat ttg agc gtt	678
Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val	
200 205 210	
tta gag act aaa gaa att gcc gct tat aga gat gcg cat tat ccc ttt	726
Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe	
215 220 225	
gtt tta ctg gaa gcg agc ggg aac att tca cta gag agc att aac gct	774
Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala	
230 235 240 245	
tac gct aaa agc ggc gtg gat gcc att agc gta ggg gct tta atc cat	822
Tyr Ala Lys Ser Gly Val Asp Ala Ile Ser Val Gly Ala Leu Ile His	
250 255 260	
caa gcc act ttt att gac atg cac atg aaa atg gct taaagacttt	868
Gln Ala Thr Phe Ile Asp Met His Met Lys Met Ala	
265 270	
aaaaaggggt tattaacatg ctaaaagaat atttagaaag cattaaagat cttacgcctg	928
aaaagaatga actcacgcac cgcccttctt tatacaactt gcttaatcag ttaaaaaacc	988
at	990

<210> 186
 <211> 273
 <212> PRT
 <213> Helicobacter pylori

<400> 186
 Met Glu Ile Arg Thr Phe Leu Glu Arg Ala Leu Lys Glu Asp Leu Gly
 1 5 10 15
 His Gly Asp Leu Phe Glu Arg Val Leu Glu Lys Asp Phe Lys Ala Thr
 20 25 30
 Ala Phe Val Arg Ala Lys Gln Glu Gly Val Phe Ser Gly Glu Lys Tyr
 35 40 45
 Ala Leu Glu Leu Leu Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile
 50 55 60
 Lys Asp Lys Glu Arg Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg
 65 70 75 80
 Gly Asp Phe Ser Met Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu
 85 90 95
 Leu Gln His Ser Ser Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu
 100 105 110
 Ala Leu Asn Ser His Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg
 115 120 125
 Pro Leu Leu Arg Ile Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala
 130 135 140
 Ser Asn His Arg Leu Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr
 145 150 155 160
 His Leu Arg His Val Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg
 165 170 175
 Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe
 180 185 190
 Glu Glu Ala Lys Asn Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys
 195 200 205
 Asp Asn Leu Ser Val Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp
 210 215 220
 Ala His Tyr Pro Phe Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu
 225 230 235 240
 Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly Val Asp Ala Ile Ser Val
 245 250 255
 Gly Ala Leu Ile His Gln Ala Thr Phe Ile Asp Met His Met Lys Met
 260 265 270
 Ala

<210> 187
 <211> 1153
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1100)

<400> 187
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 Met Ile
 1
 aaa ata tct ttg aac tcc aac aag cgg gcg tgg atg tgg tgg ttt cag 104
 Lys Ile Ser Leu Asn Ser Asn Lys Arg Ala Trp Met Trp Trp Phe Gln

5					10					15					
gga gtt ata ttt tta aat cca aag atc gta agc tgg cta ttg aag gct	152														
Gly Val Ile Phe Leu Asn Pro Lys Ile Val Ser Trp Leu Leu Lys Ala															
20 25 30															
tac aga atg tca gac aat ctc ttg cat aaa gac atc caa gcc cta atc	200														
Tyr Arg Met Ser Asp Asn Leu Leu His Lys Asp Ile Gln Ala Leu Ile															
35 40 45 50															
gct cgc tta aag cgc cag gac tta agc ttg ggc atg cta gaa aaa tcg	248														
Ala Arg Leu Lys Arg Gln Asp Leu Ser Leu Gly Met Leu Glu Lys Ser															
55 60 65															
ctc tct cgc ctt att cat gat gaa atc aat ttg gag tat ttg aag gcg	296														
Leu Ser Arg Leu Ile His Asp Glu Ile Asn Leu Glu Tyr Leu Lys Ala															
70 75 80															
tgc ggg ctc aat ttc ata gaa acg agc gaa aat tta atc acg ctc aaa	344														
Cys Gly Leu Asn Phe Ile Glu Thr Ser Glu Asn Leu Ile Thr Leu Lys															
85 90 95															
aac ctt aaa acc ccc ctt aaa gat gag gtt ttt tcc ttt att gat tta	392														
Asn Leu Lys Thr Pro Leu Lys Asp Glu Val Phe Ser Phe Ile Asp Leu															
100 105 110															
gaa acc acc gga tct tgc ccc ata aag cat gag att tta gaa att ggg	440														
Glu Thr Thr Gly Ser Cys Pro Ile Lys His Glu Ile Leu Glu Ile Gly															
115 120 125 130															
gcc gtg caa gtg aaa ggg ggg gaa att atc aat cgt ttt gaa acc ctt	488														
Ala Val Gln Val Lys Gly Gly Glu Ile Ile Asn Arg Phe Glu Thr Leu															
135 140 145															
gtg aaa gtc aaa agc gtg cct gat tat atc gct gag ctt aca ggc atc	536														
Val Lys Val Lys Ser Val Pro Asp Tyr Ile Ala Glu Leu Thr Gly Ile															
150 155 160															
act tat gaa gac acc cta aac gcc cca agc gcg cat gaa gct ttg caa	584														
Thr Tyr Glu Asp Thr Leu Asn Ala Pro Ser Ala His Glu Ala Leu Gln															
165 170 175															
gaa ttg cgg ctt ttt tta ggc aat agc gtg ttt gtg gcc cac aac gct	632														
Glu Leu Arg Leu Phe Leu Gly Asn Ser Val Phe Val Ala His Asn Ala															
180 185 190															
aat ttt gat tac aac ttt ttg ggg cgt tat ttt gta gaa aaa ttg cat	680														
Asn Phe Asp Tyr Asn Phe Leu Gly Arg Tyr Phe Val Glu Lys Leu His															
195 200 205 210															
tgc cct tta ttg aat tta aag ctt tgc act ctg gat tta tcc aaa cga	728														
Cys Pro Leu Leu Asn Leu Lys Leu Cys Thr Leu Asp Leu Ser Lys Arg															
215 220 225															
gcc att ttg tcc atg cgt tat tct ttg agc ttt tta aaa gag ctt tta	776														
Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu Leu Leu															
230 235 240															
ggg ttt ggt ata gaa gtc agc cat aga gcc tat gcg gac gct tta gcg	824														

Gly	Phe	Gly	Ile	Glu	Val	Ser	His	Arg	Ala	Tyr	Ala	Asp	Ala	Leu	Ala		
		245					250					255					
agc	tat	aaa	ctc	ttt	gaa	ata	tgc	ctg	tta	aac	ttg	ccc	agc	tac	atc	872	
Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu	Leu	Asn	Leu	Pro	Ser	Tyr	Ile		
	260					265					270						
aaa	acg	aca	atg	gat	ttg	att	gat	ttt	tct	aaa	tgt	gct	aac	acg	cta	920	
Lys	Thr	Thr	Met	Asp	Leu	Ile	Asp	Phe	Ser	Lys	Cys	Ala	Asn	Thr	Leu		
275					280					285					290		
atc	aaa	aga	ccc	cca	aaa	gcc	aga	tac	caa	gag	att	cca	tcg	cca	ttt	968	
Ile	Lys	Arg	Pro	Pro	Lys	Ala	Arg	Tyr	Gln	Glu	Ile	Pro	Ser	Pro	Phe		
			295						300					305			
tct	ctt	ttt	gaa	aag	aca	aag	ggc	ttg	ttc	aat	cat	aaa	agc	aac	cag	1016	
Ser	Leu	Phe	Glu	Lys	Thr	Lys	Gly	Leu	Phe	Asn	His	Lys	Ser	Asn	Gln		
			310					315					320				
tta	aac	gaa	agc	tgt	tta	atg	ggg	ttt	atg	ggg	act	gaa	att	tta	gca	1064	
Leu	Asn	Glu	Ser	Cys	Leu	Met	Gly	Phe	Met	Gly	Thr	Glu	Ile	Leu	Ala		
		325					330					335					
tct	cta	ttt	gat	act	ttt	gaa	tgt	tgc	cta	gta	ttt	tgatttttattc				1110	
Ser	Leu	Phe	Asp	Thr	Phe	Glu	Cys	Cys	Leu	Val	Phe						
	340					345					350						
ggttacttcg	cactcatcgt	atatcttttt	gtattctttgt	atg												1153	
		<210>	188														
		<211>	350														
		<212>	PRT														
		<213>	Helicobacter pylori														
		<400>	188														
Met	Ile	Lys	Ile	Ser	Leu	Asn	Ser	Asn	Lys	Arg	Ala	Trp	Met	Trp	Trp		
1				5					10					15			
Phe	Gln	Gly	Val	Ile	Phe	Leu	Asn	Pro	Lys	Ile	Val	Ser	Trp	Leu	Leu		
			20					25					30				
Lys	Ala	Tyr	Arg	Met	Ser	Asp	Asn	Leu	Leu	His	Lys	Asp	Ile	Gln	Ala		
		35					40					45					
Leu	Ile	Ala	Arg	Leu	Lys	Arg	Gln	Asp	Leu	Ser	Leu	Gly	Met	Leu	Glu		
	50					55					60						
Lys	Ser	Leu	Ser	Arg	Leu	Ile	His	Asp	Glu	Ile	Asn	Leu	Glu	Tyr	Leu		
65				70						75					80		
Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser	Glu	Asn	Leu	Ile	Thr		
			85					90						95			
Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu	Val	Phe					

Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg Tyr Phe Val Glu Lys
 195 200 205
 Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys Thr Leu Asp Leu Ser
 210 215 220
 Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu
 225 230 235 240
 Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg Ala Tyr Ala Asp Ala
 245 250 255
 Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu Leu Asn Leu Pro Ser
 260 265 270
 Tyr Ile Lys Thr Thr Met Asp Leu Ile Asp Phe Ser Lys Cys Ala Asn
 275 280 285
 Thr Leu Ile Lys Arg Pro Pro Lys Ala Arg Tyr Gln Glu Ile Pro Ser
 290 295 300
 Pro Phe Ser Leu Phe Glu Lys Thr Lys Gly Leu Phe Asn His Lys Ser
 305 310 315 320
 Asn Gln Leu Asn Glu Ser Cys Leu Met Gly Phe Met Gly Thr Glu Ile
 325 330 335
 Leu Ala Ser Leu Phe Asp Thr Phe Glu Cys Cys Leu Val Phe
 340 345 350

<210> 189
 <211> 990
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (52)...(864)

<400> 189
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 Met Ala
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 aaa att gaa agc aat gat tcc cac cta aga ggt att tta aaa gac gaa 105
 Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys Asp Glu
 5 10 15
 ctc tac tat caa atc ccc atc tac caa cgc cct tat caa tgg aca gaa 153
 Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp Thr Glu
 20 25 30
 gaa aac tgc gaa aaa ctt tta gac gat ttg ttt ttt aat tat gaa gat 201
 Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr Glu Asp
 35 40 45 50
 gac aga gaa ggc gat tat ttt tgc ggc tca tta gtc tta att gca atc 249
 Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile Ala Ile
 55 60 65
 agc aaa gat tct aaa gcc aca acc tat gat gtt gta gat ggc cag caa 297
 Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly Gln Gln
 70 75 80
 cgc tta agc act ttc att ctg ctt gca aaa gtt tta gcc gat ctt tat 345
 Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp Leu Tyr
 85 90 95

aat gat tgt tta gac cct aag aat tta gaa cat tta caa gag ggt tgg	393
Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu Gly Trp	
100 105 110	
aaa gat agg cat aca gaa aga aaa cga ctg agt ttt aac act ata ggg	441
Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr Ile Gly	
115 120 125 130	
tct aac gct gaa tat gat ttt caa gat gca tta gaa cat ttc aac gac	489
Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe Asn Asp	
135 140 145	
tct caa gca agc aag aat aaa aat aat aag aac aat tac cta aaa aat	537
Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu Lys Asn	
150 155 160	
gcg atc tgt tta aaa gac tat ctc atg aaa aaa gag att aaa aac att	585
Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys Asn Ile	
165 170 175	
aac gat ttc att gag tgg ctg tat tct aat gtt aaa ttt atc acc atc	633
Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile Thr Ile	
180 185 190	
att tgc cca aac ata gac aag gca tta agg att ttt aat gtt tta aac	681
Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val Leu Asn	
195 200 205 210	
gct agg ggt ttg cct ttg aat gcg aca gat att ttt aag ggg gaa tta	729
Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly Glu Leu	
215 220 225	
tta aaa cac gct aaa gag cat gag cga gaa gaa ttt gtg tct cgt tgg	777
Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser Arg Trp	
230 235 240	
aac gcc tta agc caa aaa tgc tcg gac aat gat tta aca atg gag aca	825
Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met Glu Thr	
245 250 255	
tta ttc agt tgg tat aac cta tct caa tcc ggt aac ttc tagagacaaa	874
Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe	
260 265 270	
atggaaaaag agctcgttac ttggttcaac atacttaaca aacccccctt agaatacctt	934
aagggcgtag aggattttta caacgcttat ggtgaggtgt tagaaatgca agatcg	990

<210> 190

<211> 271

<212> PRT

<213> Helicobacter pylori

<400> 190

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Asp Glu Leu Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp	
20 25 30	
Thr Glu Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr	
35 40 45	

Glu Asp Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile
50 55 60
Ala Ile Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly
65 70 75 80
Gln Gln Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp
85 90 95
Leu Tyr Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu
100 105 110
Gly Trp Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr
115 120 125
Ile Gly Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe
130 135 140
Asn Asp Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu
145 150 155 160
Lys Asn Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys
165 170 175
Asn Ile Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile
180 185 190
Thr Ile Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val
195 200 205
Leu Asn Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly
210 215 220
Glu Leu Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser
225 230 235 240
Arg Trp Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met
245 250 255
Glu Thr Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe
260 265 270

<210> 191
<211> 283
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(230)

<400> 191
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Met Val
1
gct ggg ggg cgt gaa gtg gtg ttt aaa gat aat gac aaa aag gaa gcc 104
Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys Glu Ala
5 10 15
aag ctt ttt gaa tac ggc atc aat gcg gtg gtg cta ggg gac tat ttg 152
Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp Tyr Leu
20 25 30
acc acc aaa ggc aaa gcc cct aaa aaa gat ata gaa aaa ctg ctc tct 200
Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu Leu Ser
35 40 45 50
tat ggc ttg aca atg gcg aca agc tgt cat taatgagaga acttttttaa 250
Tyr Gly Leu Thr Met Ala Thr Ser Cys His
55 60

agcggttagag gggttttttcg ccttcttaga atg

283

<210> 192
 <211> 60
 <212> PRT
 <213> Helicobacter pylori

<400> 192
 Met Val Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys
 1 5 10 15
 Glu Ala Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp
 20 25 30
 Tyr Leu Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu
 35 40 45
 Leu Ser Tyr Gly Leu Thr Met Ala Thr Ser Cys His
 50 55 60

<210> 193
 <211> 478
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(425)

<400> 193
 cacttggttg gagtgcctat aggcataata agtcctgttt ctatttttaa tgg tgg 56
 Trp Trp
 1
 tat gat aac aat gtc aac tta cag ctt ttt tat gga ttt tta cac aat 104
 Tyr Asp Asn Asn Val Asn Leu Gln Leu Phe Tyr Gly Phe Leu His Asn
 5 10 15
 gtg tat gaa aat gag aag ttt ttc atc ggt tat ttt ata ggg gct ggg 152
 Val Tyr Glu Asn Glu Lys Phe Phe Ile Gly Tyr Phe Ile Gly Ala Gly
 20 25 30
 cta ggg ggt gag agc gta aca ccc aat gtt ctt aaa gat ttt ggt aat 200
 Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe Gly Asn
 35 40 45 50
 atg tta gcg caa tta gtg caa ttt cag ggc tat ggc tca cta ggg cta 248
 Met Leu Ala Gln Leu Val Gln Phe Gln Gly Tyr Gly Ser Leu Gly Leu
 55 60 65
 agg atg ggc gat aaa cac cac acg cta gaa ttg agc acg agc gtt cat 296
 Arg Met Gly Asp Lys His His Thr Leu Glu Leu Ser Thr Ser Val His
 70 75 80
 ggc gac gct cct agt tgt tct tta aaa aag cta aag agt tgc gaa agt 344
 Gly Asp Ala Pro Ser Cys Ser Leu Lys Lys Leu Lys Ser Cys Glu Ser
 85 90 95
 gcg agg gtt tta caa gca aaa atc cct agg ggc att ttt gaa agc tat 392
 Ala Arg Val Leu Gln Ala Lys Ile Pro Arg Gly Ile Phe Glu Ser Tyr
 100 105 110

ggt act tgg agc gcg gat tat gtt tat cgt ttt taaaagt ttt taaaaattta 445
Val Thr Trp Ser Ala Asp Tyr Val Tyr Arg Phe
115 120 125

atggctttgt tccaattgaa taggggtaat aaa 478

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<210> 194
<211> 125
<212> PRT
<213> Helicobacter pylori
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His	Asn	Val	Tyr 20	Glu	Asn	Glu	Lys	Phe 25	Phe	Ile	Gly	Tyr	Phe 30	Ile	Gly
Ala	Gly	Leu 35	Gly	Gly	Glu	Ser	Val 40	Thr	Pro	Asn	Val	Leu 45	Lys	Asp	Phe
Gly	Asn 50	Met	Leu	Ala	Gln 55	Leu	Val	Gln	Phe	Gln	Gly 60	Tyr	Gly	Ser	Leu
Gly 65	Leu	Arg	Met	Gly	Asp 70	Lys	His	His	Thr	Leu	Glu 75	Leu	Ser	Thr 80	Ser
Val	His	Gly	Asp	Ala 85	Pro	Ser	Cys	Ser	Leu 90	Lys	Lys	Leu	Lys	Ser 95	Cys
Glu	Ser	Ala	Arg 100	Val	Leu	Gln	Ala	Lys 105	Ile	Pro	Arg	Gly	Ile 110	Phe	Glu
Ser	Tyr	Val 115	Thr	Trp	Ser	Ala	Asp 120	Tyr	Val	Tyr	Arg	Phe 125			

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<210> 195
<211> 2169
<212> DNA
<213> Helicobacter pylori
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<220>
<221> CDS
<222> (53) ... (2119)
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<400> 195
cttttaaaag gctaatgcct ttttaaaaaa ttgaaataaa ggaataaaag tt atg acg 58
Met Thr
1

gat aac aac caa aac aat gaa aac cat gaa aac agc agt gaa aat tca 106
Asp Asn Asn Gln Asn Asn Glu Asn His Glu Asn Ser Ser Glu Asn Ser
5 10 15

aaa gct gat gag atg cga gcc gga gcg ttt gag cgc ttc acc aac cgc 154
Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr Asn Arg
20 25 30

aaa aag cgt ttc aga gaa aac gcg caa aaa aac gca gag tat tca aac 202
Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr Ser Asn
35 40 45 50

cat gaa gcg tct tcg cac cat aaa aaa gag cat cgc cct aac aaa aaa 250
His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn Lys Lys
55 60 65

cca aac aac cac cac aaa caa aaa cat gcc aaa aca cga aat tac gcc	298
Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn Tyr Ala	
70 75 80	
caa gaa gaa ttg gat agc aac aaa gta gag ggc gtt acg gaa att ttg	346
Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu Ile Leu	
85 90 95	
cat gtg aat gag aga ggg act tta ggc ttt cat aag gag tta aaa aag	394
His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu Lys Lys	
100 105 110	
ggc gtt gaa gcg aat aac aag atc caa gtg gag cat tta aac ccg cat	442
Gly Val Glu Ala Asn Asn Lys Ile Gln Val Glu His Leu Asn Pro His	
115 120 125 130	
tat aag atg aac tta aac tct aaa gcg agc gtt aaa atc acg cct tta	490
Tyr Lys Met Asn Leu Asn Ser Lys Ala Ser Val Lys Ile Thr Pro Leu	
135 140 145	
ggg ggc ttg ggt gag att ggg ggg aac atg atg gtc att gaa acc cca	538
Gly Gly Leu Gly Glu Ile Gly Gly Asn Met Met Val Ile Glu Thr Pro	
150 155 160	
aaa agc gcg atc gtg att gat gcg ggc atg agc ttc cct aaa gag ggg	586
Lys Ser Ala Ile Val Ile Asp Ala Gly Met Ser Phe Pro Lys Glu Gly	
165 170 175	
ctc ttt ggc gtg gat att tta atc ccg gat ttt tcc tac ttg cac caa	634
Leu Phe Gly Val Asp Ile Leu Ile Pro Asp Phe Ser Tyr Leu His Gln	
180 185 190	
atc aag gac aaa atc gct ggc att atc atc acc cat gcc cat gaa gat	682
Ile Lys Asp Lys Ile Ala Gly Ile Ile Ile Thr His Ala His Glu Asp	
195 200 205 210	
cac ata ggg gcc acg cct tat ttg ttt aaa gag ctg caa ttc ccc ctt	730
His Ile Gly Ala Thr Pro Tyr Leu Phe Lys Glu Leu Gln Phe Pro Leu	
215 220 225	
tat ggc acg ccc ttg agt ttg ggg ctg att ggg agc aag ttt gat gaa	778
Tyr Gly Thr Pro Leu Ser Leu Gly Leu Ile Gly Ser Lys Phe Asp Glu	
230 235 240	
cat ggt ttg aaa aaa tac cgc tcg tat ttt aaa atc gta gaa aag cgc	826
His Gly Leu Lys Lys Tyr Arg Ser Tyr Phe Lys Ile Val Glu Lys Arg	
245 250 255	
tgt ccc att agc gtg ggc gaa ttt atc att gaa tgg atc cac atc acg	874
Cys Pro Ile Ser Val Gly Glu Phe Ile Ile Glu Trp Ile His Ile Thr	
260 265 270	
cat tct atc att gac agc agc gct tta gcg atc caa act aaa gcc gga	922
His Ser Ile Ile Asp Ser Ser Ala Leu Ala Ile Gln Thr Lys Ala Gly	
275 280 285 290	
acg atc atc cac acc ggc gat ttt aaa atc gat cac acc ccg gtg gat	970
Thr Ile Ile His Thr Gly Asp Phe Lys Ile Asp His Thr Pro Val Asp	
295 300 305	

535	540	545	
atc tat tta atg gag gat ggc gat cag gtg gag gtt ggc cct gcg ttc Ile Tyr Leu Met Glu Asp Gly Asp Gln Val Glu Val Gly Pro Ala Phe 550 555 560			1738
atc aaa aaa gtc ggc acg att aaa agc ggg aaa agc tat gtg gat aac Ile Lys Lys Val Gly Thr Ile Lys Ser Gly Lys Ser Tyr Val Asp Asn 565 570 575			1786
caa agc aat ttg agt att gat aca agc atc gtg caa caa aga gaa gaa Gln Ser Asn Leu Ser Ile Asp Thr Ser Ile Val Gln Gln Arg Glu Glu 580 585 590			1834
gtc gct agc gcc ggg gtg ttt gtg gct acg att ttt gtg aat aaa aac Val Ala Ser Ala Gly Val Phe Val Ala Thr Ile Phe Val Asn Lys Asn 595 600 605 610			1882
aag caa gcg ctt tta gaa agc tct caa ttt tcc agt tta ggg ctt gtg Lys Gln Ala Leu Leu Glu Ser Ser Gln Phe Ser Ser Leu Gly Leu Val 615 620 625			1930
ggg ttc aaa gat gaa aag cct ttg atc aaa gaa att caa ggg ggc tta Gly Phe Lys Asp Glu Lys Pro Leu Ile Lys Glu Ile Gln Gly Gly Leu 630 635 640			1978
gag gtg tta ttg aaa tcc agc aac gcc gaa att ttg aat aac cct aaa Glu Val Leu Leu Lys Ser Ser Asn Ala Glu Ile Leu Asn Asn Pro Lys 645 650 655			2026
aaa tta gaa gat cac act cgt aat ttc atc aga aaa gcg ctc ttt aaa Lys Leu Glu Asp His Thr Arg Asn Phe Ile Arg Lys Ala Leu Phe Lys 660 665 670			2074
aag ttt aga aaa tac ccg gct atc att tgt cat gcc cat tct ttt Lys Phe Arg Lys Tyr Pro Ala Ile Ile Cys His Ala His Ser Phe 675 680 685			2119
tgattgtaac gctattgctt cacaagtttt aaaagatgaa gcgagcgcg			2169
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<211> 689			
<212> PRT			
<213> Helicobacter pylori			
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Asn Ser Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr 20 25 30			
Asn Arg Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr 35 40 45			
Ser Asn His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn 50 55 60			
Lys Lys Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn 65 70 75 80			
Tyr Ala Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu 85 90 95			
Ile Leu His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu			

atc acc cca agc aac cac aac aca gaa ggt ttt aaa cat gct tta gac Ile Thr Pro Ser Asn His Asn Thr Glu Gly Phe Lys His Ala Leu Asp 120 125 130	441
gcg ttt aaa gcc atg agc aaa tcc cat aaa ttc gtt ttt gac ttt aaa Ala Phe Lys Ala Met Ser Lys Ser His Lys Phe Val Phe Asp Phe Lys 135 140 145	489
acc caa agc caa gaa tgc aaa gaa ttt atc aaa aac cgt tta aat tct Thr Gln Ser Gln Glu Cys Lys Glu Phe Ile Lys Asn Arg Leu Asn Ser 150 155 160	537
agc cat tta ctc agc aaa atc caa att gac aaa aac aat ttc ttt acg Ser His Leu Leu Ser Lys Ile Gln Ile Asp Lys Asn Asn Phe Phe Thr 165 170 175 180	585
atc tat caa aag tgg ctt gaa att gtc aaa ccc acc att gac ata aat Ile Tyr Gln Lys Trp Leu Glu Ile Val Lys Pro Thr Ile Asp Ile Asn 185 190 195	633
tgg gag gtg gct aaa act aaa gac att tta gac gca gac tat tat tta Trp Glu Val Ala Lys Thr Lys Asp Ile Leu Asp Ala Asp Tyr Tyr Leu 200 205 210	681
gcg gat ttg ctt agc gat ggc gat aaa acc att att gag aaa ttg cac Ala Asp Leu Leu Ser Asp Gly Asp Lys Thr Ile Ile Glu Lys Leu His 215 220 225	729
acg att tta aga tcg agc cat tat aaa ttg aat agg ggt gtg aat gaa Thr Ile Leu Arg Ser Ser His Tyr Lys Leu Asn Arg Gly Val Asn Glu 230 235 240	777
tta ggc aaa atg gat ttt atg gaa gtt ggt ttc aca gac agc caa caa Leu Gly Lys Met Asp Phe Met Glu Val Gly Phe Thr Asp Ser Gln Gln 245 250 255 260	825
gcc cat caa gaa ttt tgg agc gtt tat gaa cga ccg cct aaa aga gaa Ala His Gln Glu Phe Trp Ser Val Tyr Glu Arg Pro Pro Lys Arg Glu 265 270 275	873
ttt caa gcc tct att tta gag cgg cgc gac ttg tta gta cca agc gat Phe Gln Ala Ser Ile Leu Glu Arg Arg Asp Leu Leu Val Pro Ser Asp 280 285 290	921
gtg aga gaa agg aaa ggg gcg ttt ttc acc cct aaa atc tgg gta gaa Val Arg Glu Arg Lys Gly Ala Phe Thr Pro Lys Ile Trp Val Glu 295 300 305	969
aag agt caa gaa tat tta gct aaa gct ttg ggg caa gat tat caa gag Lys Ser Gln Glu Tyr Leu Ala Lys Ala Leu Gly Gln Asp Tyr Gln Glu 310 315 320	1017
gat tgt atc att tgg gat tgc gct ggg ggg act ggg aat ttg ctt cga Asp Cys Ile Ile Trp Asp Cys Ala Gly Gly Thr Gly Asn Leu Leu Arg 325 330 335 340	1065
ggt tta ttg aat aag gct aat ttg tat cta tcc act tta gat cat aac Gly Leu Leu Asn Lys Ala Asn Leu Tyr Leu Ser Thr Leu Asp His Asn 345 350 355	1113

585										590					595					
gcc	ccc	ttt	gaa	acc	cct	tta	cac	act	gtt	agt	tta	gaa	ata	ttt	gat	1881				
Ala	Pro	Phe	Glu	Thr	Pro	Leu	His	Thr	Val	Ser	Leu	Glu	Ile	Phe	Asp					
			600				605						610							
agt	ttc	ggc	gga	ttt	tta	ggc	agt	aaa	aaa	ata	tac	act	cac	aca	ata	1929				
Ser	Phe	Gly	Gly	Phe	Leu	Gly	Ser	Lys	Lys	Ile	Tyr	Thr	His	Thr	Ile					
			615				620						625							
gac	aaa	atg	ctt	act	tta	gcg	gat	tat	tta	caa	aag	ttt	cag	cca	aca	1977				
Asp	Lys	Met	Leu	Thr	Leu	Ala	Asp	Tyr	Leu	Gln	Lys	Phe	Gln	Pro	Thr					
			630				635						640							
aaa	aga	gac	act	att	ttt	ggc	tat	tta	gat	cct	ggt	cgc	aat	agt	ttt	2025				
Lys	Arg	Asp	Thr	Ile	Phe	Gly	Tyr	Leu	Asp	Pro	Gly	Arg	Asn	Ser	Phe					
			645				650						655			660				
caa	cat	caa	aat	cta	att	cat	att	agc	att	att	gac	aaa	tca	aaa	caa	2073				
Gln	His	Gln	Asn	Leu	Ile	His	Ile	Ser	Ile	Ile	Asp	Lys	Ser	Lys	Gln					
			665				670						675							
tcg	cat	gta	aaa	tat	ttt	cca	atc	att	gca	act	aca	att	ttg	ttg	gta	2121				
Ser	His	Val	Lys	Tyr	Phe	Pro	Ile	Ile	Ala	Thr	Thr	Ile	Leu	Leu	Val					
			680				685						690							
tct	gta	ttt	ttc	tcc	atc	cgc	cat	tgc	atc	aaa	gcc	aca	tgg	caa	aac	2169				
Ser	Val	Phe	Phe	Ser	Ile	Arg	His	Cys	Ile	Lys	Ala	Thr	Trp	Gln	Asn					
			695				700						705							
gat	agg	gat	caa	ttt	tac	gcc	ccc	tat	gac	gat	gcg	ttc	caa	gac	gac	2217				
Asp	Arg	Asp	Gln	Phe	Tyr	Ala	Pro	Tyr	Asp	Asp	Ala	Phe	Gln	Asp	Asp					
			710				715						720							
agc	gag	ttt	aaa	aac	aat	tgt	ttg	att	ttc	atg	ctt	ttt	cac	acc	cag	2265				
Ser	Glu	Phe	Lys	Asn	Asn	Cys	Leu	Ile	Phe	Met	Leu	Phe	His	Thr	Gln					
			725				730						735			740				
aac	cgc	atc	act	acc	gct	caa	ggg	act	aac	cat	ttt	atc	ccc	ttt	agc	2313				
Asn	Arg	Ile	Thr	Thr	Ala	Gln	Gly	Thr	Asn	His	Phe	Ile	Pro	Phe	Ser					
			745				750						755							
gaa	act	gaa	gtc	aat	gcc	aaa	gaa	aga	tat	tct	agc	cac	gct	cta	tta	2361				
Glu	Thr	Glu	Val	Asn	Ala	Lys	Glu	Arg	Tyr	Ser	Ser	His	Ala	Leu	Leu					
			760				765						770							
gag	ttt	tta	aaa	ggc	gaa	atc	aaa	gaa	ctt	aaa	gag	aac	gat	agc	ctc	2409				
Glu	Phe	Leu	Lys	Gly	Glu	Ile	Lys	Glu	Leu	Lys	Glu	Asn	Asp	Ser	Leu					
			775				780						785							
ttt	tta	agt	gcc	aaa	aaa	gaa	aac	aag	ccc	ctg	aaa	ttc	agc	ccg	agc	2457				
Phe	Leu	Ser	Ala	Lys	Lys	Glu	Asn	Lys	Pro	Leu	Lys	Phe	Ser	Pro	Ser					
			790				795						800							
gct	tca	aag	gtg	ttt	gac	gct	agc	aga	gag	gtt	tat	cgc	tat	tac	cac	2505				
Ala	Ser	Lys	Val	Phe	Asp	Ala	Ser	Arg	Glu	Val	Tyr	Arg	Tyr	Tyr	His					
			805				810						815			820				
aca	caa	gat	ttc	aca	aac	cgc	ccc	tat	aac	gct	aac	gca	agc	ctt	tat	2553				

Asp	Ser	Gln	Gln	Ala	His	Gln	Glu	Phe	Trp	Ser	Val	Tyr	Glu	Arg	Pro	
			260					265					270			
Pro	Lys	Arg	Glu	Phe	Gln	Ala	Ser	Ile	Leu	Glu	Arg	Arg	Asp	Leu	Leu	
		275					280					285				
Val	Pro	Ser	Asp	Val	Arg	Glu	Arg	Lys	Gly	Ala	Phe	Phe	Thr	Pro	Lys	
	290					295					300					
Ile	Trp	Val	Glu	Lys	Ser	Gln	Glu	Tyr	Leu	Ala	Lys	Ala	Leu	Gly	Gln	
305					310					315					320	
Asp	Tyr	Gln	Glu	Asp	Cys	Ile	Ile	Trp	Asp	Cys	Ala	Gly	Gly	Thr	Gly	
				325					330					335		
Asn	Leu	Leu	Arg	Gly	Leu	Leu	Asn	Lys	Ala	Asn	Leu	Tyr	Leu	Ser	Thr	
			340					345					350			
Leu	Asp	His	Asn	Asp	Val	Ala	Ile	Val	Lys	Asp	Leu	Ala	Ala	Lys	Asn	
		355					360					365				
His	Leu	Lys	Leu	Leu	Glu	Asn	His	Val	Phe	Gln	Phe	Asp	Phe	Leu	Asn	
	370					375					380					
Asp	Asp	Phe	Phe	Ser	Asp	Lys	Thr	Pro	Lys	Ser	Leu	Gln	Glu	Ile	Leu	
385					390					395					400	
Lys	Asp	Lys	Glu	Lys	Arg	Lys	Lys	Leu	Ile	Ile	Tyr	Ile	Asn	Pro	Pro	
				405					410					415		
Tyr	Ala	Glu	Ala	Gly	Asn	Lys	Ser	Lys	Met	Ser	Gly	Thr	Gly	Glu	His	
			420					425					430			
Lys	Ala	Lys	Val	Ala	Arg	Asp	Asn	Leu	Ile	Cys	Glu	Lys	Tyr	Lys	Asn	
		435					440					445				
Glu	Leu	Gly	Lys	Ala	Asn	Asn	Glu	Val	Phe	Ala	Gln	Phe	Phe	Met	Arg	
	450					455					460					
Ile	Tyr	Lys	Glu	Leu	Asn	Gly	Val	Ile	Leu	Ala	Ser	Phe	Ser	Thr	Leu	
465					470					475					480	
Lys	Asn	Leu	Gln	Gly	Ser	Asn	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Phe	Lys	
				485					490					495		
Ala	Lys	Phe	Leu	Glu	Gly	Phe	Met	Val	Pro	Ala	Asp	Thr	Phe	Asp	Asn	
			500					505					510			
Val	Arg	Gly	Gln	Phe	Pro	Ile	Gly	Phe	Leu	Val	Trp	Asp	Thr	Ser	Ser	
			515				520					525				
Ile	Leu	Pro	Lys	Glu	Asn	Pro	Leu	Asn	Leu	Gly	Gly	Asn	Ser	Lys	Glu	
	530					535					540					
Glu	Lys	Gln	Asn	Ser	Asn	Leu	Ile	Leu	Asp	Gln	Asp	Asn	Leu	Lys	Asp	
545					550					555					560	
Asn	Pro	Leu	Lys	Glu	Arg	Phe	Cys	Leu	Leu	Asp	Ile	Asn	Ala	Pro	Asn	
				565					570					575		
Arg	Lys	Met	Cys	Ser	Gln	Ser	Arg	Thr	Arg	Thr	Lys	Gly	Thr	Gln	Lys	
			580					585					590			
His	Ser	Thr	Ala	Ala	Pro	Phe	Glu	Thr	Pro	Leu	His	Thr	Val	Ser	Leu	
		595					600					605				
Glu	Ile	Phe	Asp	Ser	Phe	Gly	Gly	Phe	Leu	Gly	Ser	Lys	Lys	Ile	Tyr	
	610					615					620					
Thr	His	Thr	Ile	Asp	Lys	Met	Leu	Thr	Leu	Ala	Asp	Tyr	Leu	Gln	Lys	
625					630					635					640	
Phe	Gln	Pro	Thr	Lys	Arg	Asp	Thr	Ile	Phe	Gly	Tyr	Leu	Asp	Pro	Gly	
				645					650					655		
Arg	Asn	Ser	Phe	Gln	His	Gln	Asn	Leu	Ile	His	Ile	Ser	Ile	Ile	Asp	
			660					665					670			
Lys	Ser	Lys	Gln	Ser	His	Val	Lys	Tyr	Phe	Pro	Ile	Ile	Ala	Thr	Thr	
		675					680					685				
Ile	Leu	Leu	Val	Ser	Val	Phe	Ser	Ile	Arg	His	Cys	Ile	Lys	Ala		
	690					695				700						
Thr	Trp	Gln	Asn	Asp	Arg	Asp	Gln	Phe	Tyr	Ala	Pro	Tyr	Asp	Asp	Ala	
705					710					715					720	
Phe	Gln	Asp	Asp	Ser	Glu	Phe	Lys	Asn	Asn	Cys	Leu	Ile	Phe	Met	Leu	

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              725              730              735
Phe His Thr Gln Asn Arg Ile Thr Thr Ala Gln Gly Thr Asn His Phe
              740              745              750
Ile Pro Phe Ser Glu Thr Glu Val Asn Ala Lys Glu Arg Tyr Ser Ser
              755              760              765
His Ala Leu Leu Glu Phe Leu Lys Gly Glu Ile Lys Glu Leu Lys Glu
              770              775              780
Asn Asp Ser Leu Phe Leu Ser Ala Lys Lys Glu Asn Lys Pro Leu Lys
785              790              795              800
Phe Ser Pro Ser Ala Ser Lys Val Phe Asp Ala Ser Arg Glu Val Tyr
              805              810              815
Arg Tyr Tyr His Thr Gln Asp Phe Thr Asn Arg Pro Tyr Asn Ala Asn
              820              825              830
Ala Ser Leu Tyr Asp Ile Lys Glu Phe Phe Gln Gly Arg Asn Lys Gln
              835              840              845
Gly Lys Leu Asn Leu Pro Ala Lys Ala Lys Asp Glu Tyr Tyr Lys Gln
              850              855              860
Leu Tyr Ala Asn Leu Gln Asp Ala Leu Lys Asp Leu Ala Lys Glu Ile
865              870              875              880
Gln Pro Lys Val Tyr Glu Tyr Gly Phe Leu Arg Glu
              885              890

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<210> 199
 <211> 996
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (70)...(948)

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gagataaag atg tta gaa ttt att tta aaa att caa gct aga gac tct aaa      111
      Met Leu Glu Phe Ile Leu Lys Ile Gln Ala Arg Asp Ser Lys
              1              5              10

ggc ttg gtg agc acg att agc acc act atc gct aac aag ggc tat aac      159
Gly Leu Val Ser Thr Ile Ser Thr Thr Ile Ala Asn Lys Gly Tyr Asn
      15              20              25              30

atc gtc aaa aac gat gaa ttt gtt gat ccc tta aaa cag cgt ttt ttc      207
Ile Val Lys Asn Asp Glu Phe Val Asp Pro Leu Lys Gln Arg Phe Phe
              35              40              45

atg cgg tta aaa atc caa aaa gaa atc aag ccc ttg aat act gaa att      255
Met Arg Leu Lys Ile Gln Lys Glu Ile Lys Pro Leu Asn Thr Glu Ile
              50              55              60

aaa gag caa gaa gag caa tcc tta aag acc gct ctt ttt aaa gcc cta      303
Lys Glu Gln Glu Glu Gln Ser Leu Lys Thr Ala Leu Phe Lys Ala Leu
              65              70              75

gaa aac ttt aac gag tta ttg att gaa gtc att tta acg cat aaa aaa      351
Glu Asn Phe Asn Glu Leu Leu Ile Glu Val Ile Leu Thr His Lys Lys
              80              85              90

aac atc att ctg ctc gct act aaa gag agc cat tgc tta ggg gat ttg      399
Asn Ile Ile Leu Leu Ala Thr Lys Glu Ser His Cys Leu Gly Asp Leu

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1           5           10           15
Val Ser Thr Ile Ser Thr Thr Ile Ala Asn Lys Gly Tyr Asn Ile Val
20           25           30
Lys Asn Asp Glu Phe Val Asp Pro Leu Lys Gln Arg Phe Phe Met Arg
35           40           45
Leu Lys Ile Gln Lys Glu Ile Lys Pro Leu Asn Thr Glu Ile Lys Glu
50           55           60
Gln Glu Glu Gln Ser Leu Lys Thr Ala Leu Phe Lys Ala Leu Glu Asn
65           70           75           80
Phe Asn Glu Leu Leu Ile Glu Val Ile Leu Thr His Lys Lys Asn Ile
85           90           95
Ile Leu Leu Ala Thr Lys Glu Ser His Cys Leu Gly Asp Leu Leu Leu
100          105          110
Arg Val Tyr Gly Gly Glu Leu Asn Ala Gln Ile Leu Gly Val Ile Ser
115          120          125
Asn His Glu Ile Leu Arg Pro Leu Val Glu Lys Phe Asp Ile Pro Tyr
130          135          140
Phe Tyr Ala Pro Cys Asp Asn Gln Val Leu His Glu Lys Glu Val Leu
145          150          155          160
Glu Ile Ile Lys Asn Leu Glu Leu Lys His Lys Val Ser Ala Asp Leu
165          170          175
Leu Val Leu Ala Lys Tyr Met Arg Ile Leu Ser His Asp Phe Thr Lys
180          185          190
Arg Tyr Glu Asn Gln Ile Leu Asn Ile His His Ser Phe Leu Pro Ala
195          200          205
Phe Ile Gly Ala Asn Pro Tyr Gln Gln Ala Phe Glu Arg Gly Val Lys
210          215          220
Val Ile Gly Ala Thr Ala His Phe Val Asn Glu Ser Leu Asp Ala Gly
225          230          235          240
Pro Ile Ile Ile Gln Asp Thr Leu Pro Ile Asn His Asn Tyr Ser Val
245          250          255
Glu Lys Met Arg Leu Ala Gly Lys Asp Ile Glu Lys Leu Val Leu Ala
260          265          270
Arg Ala Leu Lys Leu Val Leu Glu Asp Arg Val Phe Val His Glu Asn
275          280          285
Lys Thr Val Val Phe
290

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<210> 201
 <211> 882
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (48)...(824)

<400> 201

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tgg cat aaa aga tta gcg gtt ggt tgt tgt atc gtt tta ttt tca tgc      104
Trp His Lys Arg Leu Ala Val Gly Cys Cys Ile Val Leu Phe Ser Cys
5           10           15

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atg atg aac gct aat agc att caa atc gtt aga gac gat ccg ccc ctt      152
Met Met Asn Ala Asn Ser Ile Gln Ile Val Arg Asp Asp Pro Pro Leu
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[illegible]

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 <211> 259
 <212> PRT
 <213> Helicobacter pylori

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 Phe Ser Cys Met Met Asn Ala Asn Ser Ile Gln Ile Val Arg Asp Asp
 20 25 30
 Pro Pro Leu Asp Pro Thr Leu Pro Ala Trp Val Tyr Ser Val Ala Leu
 35 40 45
 Leu Lys Val Tyr Phe Ser Asp Gly Thr Tyr Lys Glu Gly Tyr Ala Thr
 50 55 60
 Leu Leu Lys Asn Gly Arg Tyr Ile Ala Ser Ser Glu Thr Leu Tyr Ser
 65 70 75 80
 Asn Gly Leu Tyr Pro Lys Thr Ile Leu Ala Lys Met Gln Asp Ser Ser
 85 90 95
 Ala Lys Glu Leu Ile Cys Ile Ala Ser Leu Arg Leu Glu Ala Met Asp
 100 105 110
 Arg Asn Gln Gly Leu Ser Leu Leu Lys Thr Ala Asp Phe Arg Asp Asp
 115 120 125
 Tyr Cys His Lys Arg Glu Glu Ser Tyr Tyr His Ala Arg Ile Tyr Thr
 130 135 140
 Lys Tyr Ala Gln Thr Phe His Ser Asn Pro Tyr Thr Asn Gln Lys Thr
 145 150 155 160
 Pro Asn Ser Asp Leu Tyr Tyr Pro Ala Leu Asn Glu Gly Asn Ser Phe
 165 170 175
 Ser Ile Gln Ile Met Gly Ile Ser Val Ala Glu Leu Leu Lys Ser Lys
 180 185 190
 Lys Phe Leu Ser Leu Asp Val Ser Phe Lys Lys Gly Ser Val Leu Trp
 195 200 205
 Gly Gly Arg Pro Tyr Phe Ser Glu Val Gly Glu Phe Met Gly Met Ala
 210 215 220
 Ser Ser Thr Leu Glu Asn Gln Glu Ser Leu Val Ile Ile Pro Lys Glu
 225 230 235 240
 Lys Ile Val Gln Phe Leu Asn Ala Leu Lys Asn Gln Asn Ile Phe Pro
 245 250 255
 Asn Ile Pro

<210> 203
 <211> 669
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (88)...(603)

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 gtctttttcgg ggtgttttttt ttttaaaa atg ttt gat aaa aaa ctt tct agt aac 114
 Met Phe Asp Lys Lys Leu Ser Ser Asn
 1 5
 gat tgg cat atc caa aaa gtg gaa atg aac cat caa gtc tat gac att 162
 Asp Trp His Ile Gln Lys Val Glu Met Asn His Gln Val Tyr Asp Ile
 10 15 20 25

[illegible][illegible][illegible]

[illegible][illegible]

[illegible]

<221> CDS

<400> 209

-237-

ttt ttt cat ttt aat aag gat ttg aga aat gga agc gct ttc ggg gac 223
 Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser Ala Phe Gly Asp
 5 10 15 20
 gat gat cat ttt cct aac gat ttg att gaa atc atg cat ttt ggg ggt 271
 Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met His Phe Gly Gly
 25 30 35
 aaa aat aga gcg cga aag caa atc cct aat atg cac cat gcc gat aat 319
 Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His His Ala Asp Asn
 40 45 50
 gtt atc ctt aga acc ctt gca ata agg gta gcg cgt gaa atg gcc ttt 367
 Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg Glu Met Ala Phe
 55 60 65
 taaaacaatg tctatatattt cttcatagct gttttcttca tccaaacaca ccatgtcttt 427
 tcgtgggggc atgatttctt tag 450

<210> 212
 <211> 68
 <212> PRT
 <213> Helicobacter pylori

<400> 212
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 Ala Phe Gly Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met
 20 25 30
 His Phe Gly Gly Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His
 35 40 45
 His Ala Asp Asn Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg
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 Glu Met Ala Phe
 65

<210> 213
 <211> 1051
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(998)

<400> 213
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gaa ttc agt ttg tgg tgc gat ttt ata gaa agg gat ttt tta gaa aac 104
 Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn
 5 10 15

gac ttt tta aag ctc att aat aag ggg gct att tgc ggg gca acg agt 152
 Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser
 20 25 30

aac cct agt ttg ttt tgc gaa gcg atc aca aaa agc gcg ttt tat aaa	200
Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Lys	
35 40 45 50	
gat gaa atc gct aaa ctc aaa ggc aaa aaa gct aaa gaa att tat gaa	248
Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu	
55 60 65	
act ctg gcg tta aag gat att tta caa gct tct agc gcg ttg atg cct	296
Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro	
70 75 80	
tta tat gaa aaa gac cct aac aat ggc tac att agc cta gaa att gac	344
Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp	
85 90 95	
cct ttt tta gaa gat gat gcc gct aaa agc att gat gaa gcc aag cgg	392
Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala Lys Arg	
100 105 110	
ttg ttc aaa aca tta aac cgc cct aat gtg atg att aaa gtc cca gcg	440
Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala	
115 120 125 130	
agt gaa agc ggg att gaa gtg gtt agc gct tta act caa gcc tct att	488
Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala Ser Ile	
135 140 145	
cct gtt aat gta act tta gtc ttt tcg cct aaa att gcc ggt gaa atc	536
Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile	
150 155 160	
gct caa atc tta gcc aaa gaa gcg caa aaa aga gcg gtc att agc gtg	584
Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile Ser Val	
165 170 175	
ttt gtc tca cga ttt gac aaa gaa ata gac cct tta gtg cca aaa aat	632
Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Lys Asn	
180 185 190	
ttg caa gct caa agc ggg att atc aac gct acc gag tgc tat tat caa	680
Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr Tyr Gln	
195 200 205 210	
att aat cag cat gcc aat aag cta aca agc acc ctt ttt gca tcc aca	728
Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala Ser Thr	
215 220 225	
ggc gtt aaa tcc aat tct tta gct aaa gat tac tac att aaa gcg ctg	776
Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu	
230 235 240	
tgt ttt aaa aac tct atc aat aca gcc cct cta gag gct tta aac gct	824
Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu Asn Ala	
245 250 255	
tat ttg ctt gac cca aac acc gag tgt caa acc cct tta aag act aca	872
Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Thr Thr	

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Phe Lys Gln Ser Phe Glu Lys Leu Leu Ser Ser Phe
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Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys Met
5 10 15

gtt tgt aaa aat ttt aat cgt aag gaa tct gtt ttg ata gct caa tct 153
Val Cys Lys Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln Ser
20 25 30

tta gat att tct aaa aaa ggt tcg gta att tta ggc gct ctt ttg agt 201
Leu Asp Ile Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Leu Ser
35 40 45

tcg tta tgg ctg aca aac ccc tta aat gcc cat gaa aag aat ggc gcg 249
Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly Ala
50 55 60 65

ttt gtg ggg att agc ttg gaa gtg ggt agg gcc gat caa aag aca aac 297
Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr Asn
70 75 80

gct tat aaa aac ggc gag ttg ttt caa gtg cct ttt ggc gat gtt tcg 345
Ala Tyr Lys Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val Ser
85 90 95

gct aat gat gat ggc aaa gtt cct gac ggg cag acc ggt ggc tgt cag 393
Ala Asn Asp Asp Gly Lys Val Pro Asp Gly Gln Thr Gly Gly Cys Gln
100 105 110

cca gct tca ggg acg cca gga acg cca ggc tac act aaa gct aac tgc 441
Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn Cys
115 120 125

gtg gtc aat tgg act tcg cgc acc atg ctt agc acc aat aaa aac att 489
Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn Ile
130 135 140 145

cct ggc cgt aac cag ccg atg tat ggg cta ggc gtg atg aca ggc tat 537
Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly Tyr
150 155 160

aag cat ttt atc ggt aaa aaa aga tgg ttt ggg ttg cgc tat tac ggc 585

Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr	Gly		
			165					170					175				
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Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala	Asn		
		180					185					190					
gct	ata	tcg	cct	ttt	tat	ttg	agc	gat	caa	aaa	gcc	gac	atg	tat	act		681
Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr	Thr		
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tat	ggg	ttt	ggc	aca	gac	atg	ctt	ttt	aac	att	ata	gat	aag	cct	aaa		729
Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro	Lys		
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Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr	Trp		
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act	aat	aat	cgt	gtg	ggg	tat	ttt	aag	gac	ggg	tat	gtt	tat	ggc	gtc		825
Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly	Val		
			245					250					255				
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Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Thr		
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tgc	ggg	gac	acg	acg	ccg	gcg	agt	tgc	aat	gtg	ggg	att	aac	cct	aat		921
Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro	Asn		
	275					280					285						
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Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr	Ile		
	290				295					300					305		
ttc	caa	ttt	tta	gtg	aat	gtg	ggc	att	aga	act	aat	att	ttt	gaa	cac		1017
Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu	His		
				310					315					320			
cat	ggc	att	gag	ttt	ggc	atc	aaa	atc	ccc	acg	ctc	cct	aac	tac	ttt		1065
His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr	Phe		
			325					330					335				
ttc	aaa	ggg	tct	act	acc	ata	aga	gcg	aaa	aaa	caa	ggc	ccg	cta	gag		1113
Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu	Glu		
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aat	ggc	caa	cca	acc	act	atc	acc	gga	gca	gaa	acc	aat	ttc	agc	tta		1161
Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser	Leu		
		355				360					365						
acc	caa	acc	tta	cgc	cgt	cag	tat	tct	atg	tat	ttg	cgc	tat	gtt	tat		1209
Thr	Gln	Thr	Leu	Arg	Arg	Gln	Tyr	Ser	Met	Tyr	Leu	Arg	Tyr	Val	Tyr		
					375				380						385		
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Thr	Phe																

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 <212> PRT
 <213> Helicobacter pylori

<400> 216

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Ser	Leu	Asp	Ile	Ser	Lys	Lys	Gly	Ser	Val	Ile	Leu	Gly	Ala	Leu	Leu
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Ala	Phe	Val	Gly	Ile	Ser	Leu	Glu	Val	Gly	Arg	Ala	Asp	Gln	Lys	Thr
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Asn	Ala	Tyr	Lys	Asn	Gly	Glu	Leu	Phe	Gln	Val	Pro	Phe	Gly	Asp	Val
				85					90					95	
Ser	Ala	Asn	Asp	Asp	Gly	Lys	Val	Pro	Asp	Gly	Gln	Thr	Gly	Gly	Cys
			100					105						110	
Gln	Pro	Ala	Ser	Gly	Thr	Pro	Gly	Thr	Pro	Gly	Tyr	Thr	Lys	Ala	Asn
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Cys	Val	Val	Asn	Trp	Thr	Ser	Arg	Thr	Met	Leu	Ser	Thr	Asn	Lys	Asn
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Tyr	Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr
				165					170					175	
Gly	Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala
			180					185					190		
Asn	Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr
		195					200					205			
Thr	Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro
	210					215					220				
Lys	Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr
225					230					235					240
Trp	Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly
				245					250					255	
Val	Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile
			260					265					270		
Thr	Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro
		275				280						285			
Asn	Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr
		290				295					300				
Ile	Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu
305					310					315					320
His	His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr
				325					330					335	
Phe	Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu
			340					345					350		
Glu	Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser
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Leu	Thr	Gln	Thr	Leu	Arg	Arg	Gln	Tyr	Ser	Met	Tyr	Leu	Arg	Tyr	Val
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Tyr	Thr	Phe													
385															

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<212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (47)...(481)

<400> 217

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Ile Tyr Pro Tyr Val Leu Val Val His Leu Leu Cys Ala Ile Ile Phe
   5                      10                      15

att ggc tac ttg ttt ttt gat ggg gta att ttc cct aat gtg aag aaa      151
Ile Gly Tyr Leu Phe Phe Asp Gly Val Ile Phe Pro Asn Val Lys Lys
  20                      25                      30                      35

atg ttt ggc gaa gag ttt gcc aat aaa gcg aat aca gga atc act caa      199
Met Phe Gly Glu Glu Phe Ala Asn Lys Ala Asn Thr Gly Ile Thr Gln
                        40                      45                      50

aga gcg atc aaa atc atg ccc tta tgc gtt tta ggg ctt gtt tta aca      247
Arg Ala Ile Lys Ile Met Pro Leu Cys Val Leu Gly Leu Val Leu Thr
      55                      60                      65

ggg ggc atg atg ctt agc caa tac atg ggg ggc gat aaa ggc tgg tgt      295
Gly Gly Met Met Leu Ser Gln Tyr Met Gly Gly Asp Lys Gly Trp Cys
      70                      75                      80

gaa acc cct ttt caa aag ata ctc atg ctt aaa gtg atc tta gcg tta      343
Glu Thr Pro Phe Gln Lys Ile Leu Met Leu Lys Val Ile Leu Ala Leu
      85                      90                      95

agc att ttt ctt ttg gtg ctt ttt tct tta tcg tgt aag ttt ttg ggc      391
Ser Ile Phe Leu Leu Val Leu Phe Ser Leu Ser Cys Lys Phe Leu Gly
  100                      105                      110                      115

aag aaa aac cct att ggt aaa tat atc cac cct atc gct cta act ttt      439
Lys Lys Asn Pro Ile Gly Lys Tyr Ile His Pro Ile Ala Leu Thr Phe
      120                      125                      130

ggc ttt tta atc gcc att tta gcc aaa acg atg tgg ttt gtt      481
Gly Phe Leu Ile Ala Ile Leu Ala Lys Thr Met Trp Phe Val
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 <213> Helicobacter pylori

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 120 125 130

 tat ctt gat tta ata ggt ttt ttt aag tcg aga gat ttt ttt gaa ccg 488
 Tyr Leu Asp Leu Ile Gly Phe Phe Lys Ser Arg Asp Phe Phe Glu Pro
 135 140 145

 aca aaa gac gat tat att gtc aaa ccg gat gtc tta agg gct ata aaa 536
 Thr Lys Asp Asp Tyr Ile Val Lys Pro Asp Val Leu Arg Ala Ile Lys
 150 155 160

 aaa tac cat aaa att gct ttt aaa tct gta tat tgg caa cag aac aaa 584
 Lys Tyr His Lys Ile Ala Phe Lys Ser Val Tyr Trp Gln Gln Asn Lys
 165 170 175

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 35 40 45
 Gln Asn Lys Ile Leu Ser Phe Ser Leu Ser Phe Phe Phe Ile Phe Phe
 50 55 60
 Phe Phe Tyr Ala Ile Phe Leu Ile Phe Tyr Gln Ile Phe Leu Trp Tyr
 65 70 75 80
 Gly Ala Lys Lys Tyr Lys Gln Asn Gln Arg Asp Ser Glu Ile Val Tyr
 85 90 95
 Asn Ile Gln Lys Phe Pro Asn Glu Ile Lys Glu Glu Leu Tyr Arg Cys
 100 105 110
 Tyr Ser Lys Lys Gln Asn Lys Ile Leu Arg Thr Lys Lys Leu Asp Asp
 115 120 125
 Leu Ile Asp Tyr Leu Asp Leu Ile Gly Phe Phe Lys Ser Arg Asp Phe
 130 135 140
 Phe Glu Pro Thr Lys Asp Asp Tyr Ile Val Lys Pro Asp Val Leu Arg
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 165 170 175
 Gln Asn Lys

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Gln	Leu	Leu	Gly	Gly	Leu	Arg	Glu	Phe	Tyr	Gln	Ala	Leu	Glu	Asn	Lys		
			70					75						80			
caa	gaa	act	atc	atc	att	gcc	ccg	att	agc	gcg	tta	ttg	cac	cct	tta		344
Gln	Glu	Thr	Ile	Ile	Ile	Ala	Pro	Ile	Ser	Ala	Leu	Leu	His	Pro	Leu		
			85					90					95				
cct	aaa	aaa	gaa	ctt	tta	gaa	agc	ttt	aaa	atc	act	ctt	tta	gaa	aaa		392
Pro	Lys	Lys	Glu	Leu	Leu	Glu	Ser	Phe	Lys	Ile	Thr	Leu	Leu	Glu	Lys		
		100					105					110					
tat	aac	ctt	aag	gat	ttg	aaa	gac	aag	ctc	ttt	tat	tat	ggc	tat	gaa		440
Tyr	Asn	Leu	Lys	Asp	Leu	Lys	Asp	Lys	Leu	Phe	Tyr	Tyr	Gly	Tyr	Glu		
	115					120					125						
att	tta	gac	tta	gtg	gaa	gtg	gaa	ggc	gaa	gcg	agc	ttt	agg	ggg	gat		488
Ile	Leu	Asp	Leu	Val	Glu	Val	Glu	Gly	Glu	Ala	Ser	Phe	Arg	Gly	Asp		
130					135					140					145		
att	gtg	gat	att	tat	gcg	cca	aat	tct	aaa	gcg	tat	cgc	ttg	agt	ttt		536
Ile	Val	Asp	Ile	Tyr	Ala	Pro	Asn	Ser	Lys	Ala	Tyr	Arg	Leu	Ser	Phe		
				150					155					160			
ttt	gac	acc	gag	tgt	gag	agc	att	aag	gaa	ttt	gat	ccc	att	act	caa		584
Phe	Asp	Thr	Glu	Cys	Glu	Ser	Ile	Lys	Glu	Phe	Asp	Pro	Ile	Thr	Gln		
			165					170					175				
atg	agc	ctt	aaa	gaa	gat	ttg	tta	gaa	att	gaa	atc	ccc	ccc	acg	ctt		632
Met	Ser	Leu	Lys	Glu	Asp	Leu	Leu	Glu	Ile	Glu	Ile	Pro	Pro	Thr	Leu		
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Phe	Ser	Leu	Asp	Glu	Ser	Ser	Tyr	Lys	Asp	Leu	Lys	Thr	Lys	Val	Glu		
	195					200					205						
caa	agc	ccc	tta	aat	agc	ttt	tct	aaa	gat	tta	acc	agt	ttt	ggg	ttg		728
Gln	Ser	Pro	Leu	Asn	Ser	Phe	Ser	Lys	Asp	Leu	Thr	Ser	Phe	Gly	Leu		
210					215					220					225		
tg	ttt	tta	gga	gaa	aaa	gca	caa	gac	tta	cta	atc	gtt	tat	aaa	agc		776
Trp	Phe	Leu	Gly	Glu	Lys	Ala	Gln	Asp	Leu	Leu	Ile	Val	Tyr	Lys	Ser		
			230					235						240			
att	ata	agt	cct	aga	gct	tta	gaa	gaa	att	caa	gaa	tta	gcg	agc	tta		824
Ile	Ile	Ser	Pro	Arg	Ala	Leu	Glu	Glu	Ile	Gln	Glu	Leu	Ala	Ser	Leu		
			245					250					255				
aac	gaa	ttg	gat	tgt	gag	cgt	ttc	aaa	ttt	tta	aag	gtt	tta	gaa	aac		872
Asn	Glu	Leu	Asp	Cys	Glu	Arg	Phe	Lys	Phe	Leu	Lys	Val	Leu	Glu	Asn		
		260					265					270					
gcg	caa	ggc	tat	gaa	gat	tta	gaa	atc	cat	gcg	cat	gcc	cta	gaa	ggc		920
Ala	Gln	Gly	Tyr	Glu	Asp	Leu	Glu	Ile	His	Ala	His	Ala	Leu	Glu	Gly		
	275					280					285						

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gaa tgc gtc atc gcc ccc ttt gtg tta aac ttt aaa acc cct gat ggg Glu Cys Val Ile Ala Pro Phe Val Leu Asn Phe Lys Thr Pro Asp Gly 325 330 335	1064
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tcc aag ctc gct ttg aat gag ttg aat ccg ggc gaa tgg gtg gtg cat Ser Lys Leu Ala Leu Asn Glu Leu Asn Pro Gly Glu Trp Val Val His 355 360 365	1160
gat gat tat ggg gtg ggc gtg ttt tct caa tta gtc cag cac agc gtt Asp Asp Tyr Gly Val Gly Val Phe Ser Gln Leu Val Gln His Ser Val 370 375 380 385	1208
tta ggg agc aag agg gat ttt tta gaa atc gct tat ttg ggc gaa gac Leu Gly Ser Lys Arg Asp Phe Leu Glu Ile Ala Tyr Leu Gly Glu Asp 390 395 400	1256
aaa ctg ctg tta ccg gta gaa aac ttg cat ctc atc gct cgc tat gtg Lys Leu Leu Leu Pro Val Glu Asn Leu His Leu Ile Ala Arg Tyr Val 405 410 415	1304
gcg caa agc gat agc gtg cca gct aaa gac cgg cta ggg aaa ggg agc Ala Gln Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly Ser 420 425 430	1352
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agc aag atc att gaa tta gcg gct gaa cgc aat ttg atc ttg ggt aaa Ser Lys Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly Lys 450 455 460 465	1448
aag atg gat gtg cat tta gcg gag ttg gaa gtc ttt aaa tcg cat gcg Lys Met Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His Ala 470 475 480	1496
ggg ttt gaa tac acc agc gat caa gaa aag gct atc gct gaa att tca Gly Phe Glu Tyr Thr Ser Asp Gln Glu Lys Ala Ile Ala Glu Ile Ser 485 490 495	1544
aag gat tta agc tct cac agg gtg atg gat aga tta ttg agt ggg gat Lys Asp Leu Ser Ser His Arg Val Met Asp Arg Leu Leu Ser Gly Asp 500 505 510	1592
gtg ggt ttt ggg aaa aca gaa gtg gcg atg cat gcg att ttt tgc gcg Val Gly Phe Gly Lys Thr Glu Val Ala Met His Ala Ile Phe Cys Ala 515 520 525	1640

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Phe Leu Asn Gly Phe Gln Ser Ala Leu Val Val Pro Thr Thr Leu Leu	
530 535 540 545	
gcg cac cag cat ttt gag act tta agg gcg cgt ttt gaa aat ttt ggc	1736
Ala His Gln His Phe Glu Thr Leu Arg Ala Arg Phe Glu Asn Phe Gly	
550 555 560	
gtt aaa gtg gct cgt ttg gac agg tat gcg agc gaa aaa aac aag ctt	1784
Val Lys Val Ala Arg Leu Asp Arg Tyr Ala Ser Glu Lys Asn Lys Leu	
565 570 575	
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Leu Lys Ala Val Glu Leu Gly Gln Val Asp Ala Leu Ile Gly Thr His	
580 585 590	
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Ala Ile Leu Gly Ala Lys Phe Lys Asn Leu Gly Leu Val Val Val Asp	
595 600 605	
gaa gag cat aaa ttt ggc gtg aaa caa aaa gaa gct tta aaa gaa ttg	1928
Glu Glu His Lys Phe Gly Val Lys Gln Lys Glu Ala Leu Lys Glu Leu	
610 615 620 625	
agt aag agc gtg cat ttt tta agc atg tcc gct acg cct atc ccg cgc	1976
Ser Lys Ser Val His Phe Leu Ser Met Ser Ala Thr Pro Ile Pro Arg	
630 635 640	
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Thr Leu Asn Met Ala Leu Ser Gln Ile Lys Gly Ile Ser Ser Leu Lys	
645 650 655	
acc ccg ccc aca gac aga aag ccc agc cgc act ttt ttg aaa gaa aag	2072
Thr Pro Pro Thr Asp Arg Lys Pro Ser Arg Thr Phe Leu Lys Glu Lys	
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Asn Asp Glu Leu Leu Lys Glu Ile Ile Tyr Arg Glu Leu Arg Arg Asn	
675 680 685	
ggg caa att ttt tac atc cat aac cac atc gct agc att tta aaa gtc	2168
Gly Gln Ile Phe Tyr Ile His Asn His Ile Ala Ser Ile Leu Lys Val	
690 695 700 705	
aaa acc aag cta gaa gat tta atc cct aaa ctc aaa atc gct att ttg	2216
Lys Thr Lys Leu Glu Asp Leu Ile Pro Lys Leu Lys Ile Ala Ile Leu	
710 715 720	
cat tcc cag att aac gct aat gag agc gaa gaa atc atg cta gag ttt	2264
His Ser Gln Ile Asn Ala Asn Glu Ser Glu Glu Ile Met Leu Glu Phe	
725 730 735	
gcc aag gga aat tat cag gtt tta tta tgc act tct att gtg gaa tca	2312
Ala Lys Gly Asn Tyr Gln Val Leu Leu Cys Thr Ser Ile Val Glu Ser	
740 745 750	
ggg att cat ttg cct aac gct aac acg atc att ata gat aat gcg caa	2360
Gly Ile His Leu Pro Asn Ala Asn Thr Ile Ile Ile Asp Asn Ala Gln	

755					760					765						
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Asn	Phe	Gly	Leu	Ala	Asp	Leu	His	Gln	Leu	Arg	Gly	Arg	Val	Gly	Arg	
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Gly	Lys	Lys	Glu	Gly	Phe	Cys	Tyr	Phe	Leu	Ile	Glu	Asp	Gln	Lys	Ser	
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Leu	Asn	Glu	Gln	Ala	Leu	Lys	Arg	Leu	Leu	Ala	Leu	Glu	Lys	Asn	Ser	
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Tyr	Leu	Gly	Ser	Gly	Glu	Ser	Val	Ala	Tyr	His	Asp	Leu	Glu	Ile	Arg	
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Gly	Gly	Gly	Asn	Leu	Leu	Gly	Gln	Asp	Gln	Ser	Gly	His	Ile	Lys	Asn	
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Gly	Val	Ser	Ala	Phe	Leu	Asn	Pro	Glu	Leu	Ile	Ala	Ser	Asp	Ser	Leu	
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Arg	Leu	Asp	Leu	Tyr	Arg	Arg	Leu	Ser	Leu	Cys	Glu	Asn	Thr	Asp	Glu	
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Val	Gly	Gln	Ile	His	Glu	Glu	Ile	Glu	Asp	Arg	Phe	Gly	Lys	Ile	Asp	
	915					920				925						
gat	ttg	agc	gct	caa	ttt	ttg	caa	atc	att	acg	ctt	aaa	att	cta	gcc	2888
Asp	Leu	Ser	Ala	Gln	Phe	Leu	Gln	Ile	Ile	Thr	Leu	Lys	Ile	Leu	Ala	
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aac	cag	ctt	ggc	atc	atc	aaa	ctt	tct	aat	ttc	aat	caa	aac	atc	acc	2936
Asn	Gln	Leu	Gly	Ile	Ile	Lys	Leu	Ser	Asn	Phe	Asn	Gln	Asn	Ile	Thr	
				950					955					960		
atc	act	tat	agc	gat	gaa	aag	aaa	gaa	agc	ctg	aaa	gcc	cca	agc	aaa	2984
Ile	Thr	Tyr	Ser	Asp	Glu	L										

Overall		Non-Hispanic White		Non-Hispanic Black		Hispanic	
Mean	SD	Mean	SD	Mean	SD	Mean	SD
Age	45.2	10.5	45.2	10.5	45.2	10.5	45.2
Gender							
Male	55.2		55.2		55.2		55.2
Female	44.8		44.8		44.8		44.8
Marital Status							
Married	65.2		65.2		65.2		65.2
Single	34.8		34.8		34.8		34.8
Divorced	10.2		10.2		10.2		10.2
Widowed	5.2		5.2		5.2		5.2
Education							
High School or Less	45.2		45.2		45.2		45.2
Some College	35.2		35.2		35.2		35.2
Bachelor's Degree	15.2		15.2		15.2		15.2
Postgraduate	4.2		4.2		4.2		4.2
Income							
<\$10,000	25.2		25.2		25.2		25.2
\$10,000-\$20,000	35.2		35.2		35.2		35.2
\$20,000-\$30,000	15.2		15.2		15.2		15.2
>\$30,000	24.2		24.2		24.2		24.2
Health Insurance							
Medicare	45.2		45.2		45.2		45.2
Medicaid	35.2		35.2		35.2		35.2
Private	15.2		15.2		15.2		15.2
None	4.2		4.2		4.2		4.2

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Val	Ile	Ser 35	Tyr	Phe	Lys	Pro	Asn 40	Thr	Lys	Ala	Ile	Leu 45	Phe	Pro	Glu
Phe	Arg 50	Ala	Lys	Lys	Asn	Asp 55	Leu	Arg	Ser	Phe 60	Phe	Glu	Glu	Phe	
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Lys	Gln	Glu	Thr	Ile 85	Ile	Ile	Ala	Pro	Ile 90	Ser	Ala	Leu	Leu	His 95	Pro
Leu	Pro	Lys	Lys 100	Glu	Leu	Leu	Glu	Ser 105	Phe	Lys	Ile	Thr	Leu 110	Leu	Glu
Lys	Tyr	Asn 115	Leu	Lys	Asp	Leu	Lys 120	Asp	Lys	Leu	Phe	Tyr 125	Tyr	Gly	Tyr
Glu	Ile 130	Leu	Asp	Leu	Val	Glu 135	Val	Glu	Gly	Glu	Ala 140	Ser	Phe	Arg	Gly
Asp 145	Ile	Val	Asp	Ile 150	Tyr	Ala	Pro	Asn	Ser	Lys 155	Ala	Tyr	Arg	Leu	Ser 160
Phe	Phe	Asp	Thr	Glu 165	Cys	Glu	Ser	Ile	Lys 170	Glu	Phe	Asp	Pro	Ile 175	Thr
Gln	Met	Ser	Leu 180	Lys	Glu	Asp	Leu	Leu 185	Glu	Ile	Glu	Ile	Pro 190	Pro	Thr
Leu	Phe	Ser 195	Leu	Asp	Glu	Ser	Ser 200	Tyr	Lys	Asp	Leu	Lys 205	Thr	Lys	Val
Glu	Gln 210	Ser	Pro	Leu	Asn	Ser 215	Phe	Ser	Lys	Asp	Leu	Thr 220	Ser	Phe	Gly
Leu 225	Trp	Phe	Leu	Gly 230	Glu	Lys	Ala	Gln	Asp	Leu 235	Leu	Ile	Val	Tyr	Lys 240
Ser	Ile	Ile	Ser	Pro 245	Arg	Ala	Leu	Glu	Glu 250	Ile	Gln	Glu	Leu	Ala 255	Ser
Leu	Asn	Glu	Leu 260	Asp	Cys	Glu	Arg	Phe 265	Lys	Phe	Leu	Lys 270	Val	Leu	Glu
Asn	Ala	Gln 275	Gly	Tyr	Glu	Asp	Leu 280	Glu	Ile	His	Ala	His 285	Ala	Leu	Glu
Gly	Phe 290	Ile	Ala	Leu	His	Ser 295	Asn	His	Lys	Ile	Thr 300	Leu	Leu	Ala	Pro
Asn 305	Lys	Thr	Ile	Leu	Asp 310	Asn	Ala	Ile	Ser	Ala 315	Leu	Asp	Ala	Gly	Asn 320
Met	Glu	Cys	Val	Ile 325	Ala	Pro	Phe	Val	Leu 330	Asn	Phe	Lys	Thr	Pro	Asp
Gly	Ile	Phe	Ile 340	Ser	Leu	Asn	Ser	Phe 345	Glu	Arg	Lys	Lys	Lys 350	Arg	Gln
Lys	Ser	Lys 355	Leu	Ala	Leu	Asn	Glu 360	Leu	Asn	Pro	Gly	Glu 365	Trp	Val	Val
His	Asp 370	Asp	Tyr	Gly	Val	Gly 375	Val	Phe	Ser	Gln	Leu 380	Val	Gln	His	Ser

Val	Leu	Gly	Ser	Lys	Arg	Asp	Phe	Leu	Glu	Ile	Ala	Tyr	Leu	Gly	Glu
385					390					395					400
Asp	Lys	Leu	Leu	Leu	Pro	Val	Glu	Asn	Leu	His	Leu	Ile	Ala	Arg	Tyr
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Val	Ala	Gln	Ser	Asp	Ser	Val	Pro	Ala	Lys	Asp	Arg	Leu	Gly	Lys	Gly
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Ser	Phe	Leu	Lys	Leu	Lys	Ala	Lys	Val	Arg	Thr	Lys	Leu	Leu	Glu	Ile
		435					440					445			
Ala	Ser	Lys	Ile	Ile	Glu	Leu	Ala	Ala	Glu	Arg	Asn	Leu	Ile	Leu	Gly
	450					455					460				
Lys	Lys	Met	Asp	Val	His	Leu	Ala	Glu	Leu	Glu	Val	Phe	Lys	Ser	His
465					470					475					480
Ala	Gly	Phe	Glu	Tyr	Thr	Ser	Asp	Gln	Glu	Lys	Ala	Ile	Ala	Glu	Ile
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Ser	Lys	Asp	Leu	Ser	Ser	His	Arg	Val	Met	Asp	Arg	Leu	Leu	Ser	Gly
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Asp	Val	Gly	Phe	Gly	Lys	Thr	Glu	Val	Ala	Met	His	Ala	Ile	Phe	Cys
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Ala	Phe	Leu	Asn	Gly	Phe	Gln	Ser	Ala	Leu	Val	Val	Pro	Thr	Thr	Leu
	530					535					540				
Leu	Ala	His	Gln	His	Phe	Glu	Thr	Leu	Arg	Ala	Arg	Phe	Glu	Asn	Phe
545					550					555					560
Gly	Val	Lys	Val	Ala	Arg	Leu	Asp	Arg	Tyr	Ala	Ser	Glu	Lys	Asn	Lys
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His	Ala	Ile	Leu	Gly	Ala	Lys	Phe	Lys	Asn	Leu	Gly	Leu	Val	Val	Val
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Arg	Thr	Leu	Asn	Met	Ala	Leu	Ser	Gln	Ile	Lys	Gly	Ile	Ser	Ser	Leu
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Lys	Thr	Pro	Pro	Thr	Asp	Arg	Lys	Pro	Ser	Arg	Thr	Phe	Leu	Lys	Glu
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Lys	Asn	Asp	Glu	Leu	Leu	Lys	Glu	Ile	Ile	Tyr	Arg	Glu	Leu	Arg	Arg
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Asn	Gly	Gln	Ile	Phe	Tyr	Ile	His	Asn	His	Ile	Ala	Ser	Ile	Leu	Lys
	690					695					700				
Val	Lys	Thr	Lys	Leu	Glu	Asp	Leu	Ile	Pro	Lys	Leu	Lys	Ile	Ala	Ile
705					710					715					720
Leu	His	Ser	Gln	Ile	Asn	Ala	Asn	Glu	Ser	Glu	Glu	Ile	Met	Leu	Glu
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Phe	Ala	Lys	Gly	Asn	Tyr	Gln	Val	Leu	Cys	Thr	Ser	Ile	Val	Glu	
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Ser	Gly	Ile	His	Leu	Pro	Asn	Ala	Asn	Thr	Ile	Ile	Ile	Asp	Asn	Ala
		755					760					765			
Gln	Asn	Phe	Gly	Leu	Ala	Asp	Leu	His	Gln	Leu	Arg	Gly	Arg	Val	Gly
	770					775					780				
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785					790					795					800
Ser	Leu	Asn	Glu	Gln	Ala	Leu	Lys	Arg	Leu	Leu	Ala	Leu	Glu	Lys	Asn
				805					810					815	
Ser	Tyr	Leu	Gly	Ser	Gly	Glu	Ser	Val	Ala	Tyr	His	Asp	Leu	Glu	Ile
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Leu	Leu	Pro	Ser	Leu	Phe	Pro	Gln	Tyr	Ser	Lys	Met	Ile	Trp	Ser	Asp		
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Val	Asp	Val	Val	Phe	Cys	Arg	Ala	Phe	Ala	Asp	Asp	Phe	Ile	Ala	Leu		
			120					125					130				
gac	aca	agc	gaa	tct	ttt	cat	ttg	agt	ggg	gtg	ata	agt	tta	gta	tca		489
Asp	Thr	Ser	Glu	Ser	Phe	His	Leu	Ser	Gly	Val	Ile	Ser	Leu	Val	Ser		
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caa	tca	gtt	aca	gag	ggg	ttt	tgg	ttt	tgc	aat	ttg	gat	tac	atg	cga		537
Gln	Ser	Val	Thr	Glu	Gly	Phe	Trp	Phe	Cys	Asn	Leu	Asp	Tyr	Met	Arg		
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Lys	His	Ser	Phe	Thr	Gln	Gln	Val	Leu	Glu	Lys	Phe	Lys	Ile	Gln	Val		
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Met	Arg	Pro	Tyr	Phe	Lys	Glu	Pro	Thr	Leu	Ile	His	His	Leu	His	Ala		
				185					190					195			
tat	att	aaa	gaa	ctt	ccc	tta	cac	tat	tgc	gtt	ctg	cct	tat	tat	tat		681
Tyr	Ile	Lys	Glu	Leu	Pro	Leu	His	Tyr	Cys	Val	Leu	Pro	Tyr	Tyr	Tyr		
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Gln	Glu	Glu	Leu	Asp	Asp	Leu	Arg	His	Lys	Ala	Ser	Leu	Pro	Ile	Arg		
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Phe	Glu	Ile	Ile	His	Gln	Asp	Lys	Pro	Asn	Glu	Phe	Ile	His	Arg	Gln		
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Gln	Ile	Pro	Tyr	Glu	Ile	Ser	Gln	Ile	Gln	Asn	Ile	Leu	Ser	Asn	Pro		
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Ile	Ile	Met	His	Tyr	Glu	Ser	Asp	Lys	Asp	Ala	Leu	Gly	Ile	Tyr	Asn		
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Gly	Lys	Pro	Trp	Glu	Phe	Pro	Leu	Gly	Asn	Gln	Tyr	His	Leu	Trp	Leu		
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Glu	Met	Leu	Ala	His	Thr	Pro	Phe	Trp	Lys	Asp	Phe	Thr	Leu	Glu	Met		
		295					300					305					
caa	aaa	aaa	cgc	ata	gaa	tac	cga	gat	att	gct	caa	aaa	atc	cat	tat		1017
Gln	Lys	Lys	Arg	Ile	Glu	Tyr	Arg	Asp	Ile	Ala	Gln	Lys	Ile	His	Tyr		
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Phe	Ser	Gln	Asp	Lys	Arg	Leu	Tyr	Glu	Val	Ser	Ile	Arg	Ser	Ile	Lys		
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 atttgcaac atg ggc aat gtg aac ccc cct aaa aca agc tat aaa gag tcc 291
 Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser
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 Leu Ser Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val
 15 20 25 30

 caa aac tta atc att tgc ggg cat agc gat tgt ggg gct tgc ggg agc 387
 Gln Asn Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser
 35 40 45

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 Val His Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile
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 gca aac tgg ata caa ttt tta gag cct gtt aaa gaa gag tta aaa aac 483
 Ala Asn Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn
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 His Pro Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu
 80 85 90

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 Arg Leu Asn Ala Arg Leu Gln Leu Asn Asn Leu Ser Tyr Asp Phe
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 Ile Gln Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His
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 Tyr Ile Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His
 130 135 140

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 Phe Phe Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu
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 35 40 45
 Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile Ala Asn
 50 55 60
 Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn His Pro
 65 70 75 80
 Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu Arg Leu
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 Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe Ile Gln
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 Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His Tyr Ile
 115 120 125
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 Met Ser Ala
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 His Gly Leu Glu Gly Val Ser Gly Leu His Phe His Thr His Cys Glu
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 Gln Asn Ala Asp Ala Leu Cys Arg Thr Leu Glu His Val Glu Lys His
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 Phe Arg Pro Tyr Leu Glu Asn Met Ala Trp Val Asn Phe Gly Gly Gly
 210 215 220
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 225 230 235 240
 Ile Lys Asp Phe Lys Glu Arg Tyr His Asn Ile Glu Val Ile Leu Glu
 245 250 255
 Pro Gly Glu Ala Ile Gly Trp Gln Cys Gly Phe Leu Ile Ala Ser Val
 260 265 270
 Ile Asp Ile Val Gln Asn Asp Gln Glu Ile Ala Ile Leu Asp Ala Ser
 275 280 285
 Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro Tyr Arg Pro Ser
 290 295 300
 Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu Ile Glu Val Glu
 305 310 315 320
 Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu Gly Gly Pro Thr
 325 330 335
 Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe Glu Thr Pro Leu
 340 345 350
 Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu His Tyr Thr Ile
 355 360 365
 Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro Ser Leu Ala Arg
 370 375 380
 Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe Ser Tyr Glu Asp
 385 390 395 400
 Tyr Lys Asn Arg Asn
 405

<210> 235
 <211> 609
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (246)...(548)

<400> 235
 gaatcttttac tttataat ttt gcctgacctt ttaaaagaac actctaataa aaatgtcttg 60
 ctcatctttac acttgcaggc tcgcatggcc caaactacga caacaaagtg ccttttaaatt 120
 ttaggggtgtt taagccttat tgctcaagcg ctgatctgtc ttcttgctcc aaagaaagcc 180
 tgattaacgc ctatgacaac accattttttt acaacgacta tctgctagat cgaaagatca 240
 ttagc atg ctt gaa aac gcc aag cag ccc gcc tta atg atc tat tta agc 290
 Met Leu Glu Asn Ala Lys Gln Pro Ala Leu Met Ile Tyr Leu Ser
 1 5 10 15

 gat cat ggc gaa agt ttg ggc gaa gaa gcg ttc tat ttg cat ggc att 338
 Asp His Gly Glu Ser Leu Gly Glu Glu Ala Phe Tyr Leu His Gly Ile
 20 25 30

 cct aaa agc atc gcc ccc aaa gaa caa tac gag atc ccc ttt atc gtt 386
 Pro Lys Ser Ile Ala Pro Lys Glu Gln Tyr Glu Ile Pro Phe Ile Val
 35 40 45

tat gct aat gag cct ttc aaa gaa aag cat tcc atc att caa acc caa 434
Tyr Ala Asn Glu Pro Phe Lys Glu Lys His Ser Ile Ile Gln Thr Gln
50 55 60

acc ccc att aat caa aat gtg att ttc cat agc gtt tta ggg gtg ttt 482
Thr Pro Ile Asn Gln Asn Val Ile Phe His Ser Val Leu Gly Val Phe
65 70 75

ttg gat ttt aaa aac cca agc gtt gtt tat cgc cct tct tta gat ctg 530
Leu Asp Phe Lys Asn Pro Ser Val Val Tyr Arg Pro Ser Leu Asp Leu
80 85 90 95

ctt aaa cac aaa aaa gag taaaataaca cgcatgaaaa aattcttatt 578
Leu Lys His Lys Lys Glu
100

taaacaaaaa ttttgtgaaa gcctgccc aa 609

<210> 236
<211> 101
<212> PRT
<213> Helicobacter pylori

<400> 236
Met Leu Glu Asn Ala Lys Gln Pro Ala Leu Met Ile Tyr Leu Ser Asp
1 5 10 15
His Gly Glu Ser Leu Gly Glu Glu Ala Phe Tyr Leu His Gly Ile Pro
20 25 30
Lys Ser Ile Ala Pro Lys Glu Gln Tyr Glu Ile Pro Phe Ile Val Tyr
35 40 45
Ala Asn Glu Pro Phe Lys Glu Lys His Ser Ile Ile Gln Thr Gln Thr
50 55 60
Pro Ile Asn Gln Asn Val Ile Phe His Ser Val Leu Gly Val Phe Leu
65 70 75 80
Asp Phe Lys Asn Pro Ser Val Val Tyr Arg Pro Ser Leu Asp Leu Leu
85 90 95
Lys His Lys Lys Glu
100

<210> 237
<211> 872
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (123)...(818)

<400> 237
agtttttagcg ataattatat cttttatggc aataaaaacga gcgtttgtaa gcaaatacggt 60
aacgctgtgc ctctcttct agccctagcc ttaggcaaag cgatcttaaa aagcttaaga 120
aa atg ata caa att tat cac gct gac gct ttt gaa atc atc aaa gac 167
Met Ile Gln Ile Tyr His Ala Asp Ala Phe Glu Ile Ile Lys Asp
1 5 10 15

ttt tac cag caa aat tta aaa gtg gat gcg atc atc acg gac cct cct 215
Phe Tyr Gln Gln Asn Leu Lys Val Asp Ala Ile Ile Thr Asp Pro Pro
20 25 30

tat aac att tcg gtt aaa aac aat ttt ccc acc cta aag agc gct aaa Tyr Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys 35 40 45	263
agg caa ggc ata gat ttt ggg gaa tgg gat aaa aat ttc aag ctt tta Arg Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu 50 55 60	311
gaa tgg atc gca cgc tac gcc ccc tta gtc aat cca aac ggc tgc atg Glu Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met 65 70 75	359
gtt att ttt tgc tct tac agg ttt ata agc tat atc gct gat ttt tta Val Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu 80 85 90 95	407
gaa gaa aac ggc ttt gtg gtc aaa gac ttt atc caa tgg gtt aaa aat Glu Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn 100 105 110	455
aat ccc atg cca aga aac att cac cgg cgt tat gtc caa gac acg gaa Asn Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu 115 120 125	503
ttt gct ctg tgg gcg gtt aaa aag aaa gcc aag tgg gtg ttt aac aaa Phe Ala Leu Trp Ala Val Lys Lys Lys Ala Lys Trp Val Phe Asn Lys 130 135 140	551
ccc aaa aat gaa aaa tat tta cgg cct ttg att tta aaa agc cct gtg Pro Lys Asn Glu Lys Tyr Leu Arg Pro Leu Ile Leu Lys Ser Pro Val 145 150 155	599
gta agc ggg ctt gaa aaa acc aaa cac ccc acg caa aaa agc ctg gcc Val Ser Gly Leu Glu Lys Thr Lys His Pro Thr Gln Lys Ser Leu Ala 160 165 170 175	647
tta atg gaa aaa atc att tcc atc cac aca aac cct aat gac atc gtg Leu Met Glu Lys Ile Ile Ser Ile His Thr Asn Pro Asn Asp Ile Val 180 185 190	695
cta gat cct ttc atg ggg agc ggc acc acc ggc tta gcg tgc aaa aat Leu Asp Pro Phe Met Gly Ser Gly Thr Thr Gly Leu Ala Cys Lys Asn 195 200 205	743
tta gaa cgg aat ttt atc ggc ata gaa tca gaa aaa gaa tat ttt caa Leu Glu Arg Asn Phe Ile Gly Ile Glu Ser Glu Lys Glu Tyr Phe Gln 210 215 220	791
acc gct aaa aag cgt ttg aat ctg ttt taaaaacgct atttgaatga Thr Ala Lys Lys Arg Leu Asn Leu Phe 225 230	838
gattgtgtta tagttattta aaaggatatt ttga	872

<210> 238

<211> 232

<212> PRT

<213> Helicobacter pylori

atc aaa cta gct aaa aaa tta gaa atc aac atg atc att ggc ggc cct Ile Lys Leu Ala Lys Lys Leu Glu Ile Asn Met Ile Ile Gly Gly Pro 65 70 75 80	299
cca tgt caa ggc ttt tct aat aaa ggg aaa aat tta ggc cta aaa gac Pro Cys Gln Gly Phe Ser Asn Lys Gly Lys Asn Leu Gly Leu Lys Asp 85 90 95	347
cct agg aat ttt tta ttc tta gaa tat ata gaa ata gtc aaa gcc ata Pro Arg Asn Phe Leu Phe Leu Glu Tyr Ile Glu Ile Val Lys Ala Ile 100 105 110	395
aag cca gaa att ttt atc att gaa aac gtg aaa aac ctc atc tct tgc Lys Pro Glu Ile Phe Ile Ile Glu Asn Val Lys Asn Leu Ile Ser Cys 115 120 125	443
gct aaa ggc tat ttt tta gaa gaa att aaa gaa agg ttg aac gct tta Ala Lys Gly Tyr Phe Leu Glu Glu Ile Lys Glu Arg Leu Asn Ala Leu 130 135 140	491
ggg tat caa ttg agc tat caa atc cta aac gct aaa gat tat ggc gtg Gly Tyr Gln Leu Ser Tyr Gln Ile Leu Asn Ala Lys Asp Tyr Gly Val 145 150 155 160	539
cct caa aac aga gag aga gcc ttt att gta ggg gct agt cgt ttc agt Pro Gln Asn Arg Glu Arg Ala Phe Ile Val Gly Ala Ser Arg Phe Ser 165 170 175	587
ttt gat ttc aat ctt tta gag cct tct caa agc gtg aat gtt caa gat Phe Asp Phe Asn Leu Leu Glu Pro Ser Gln Ser Val Asn Val Gln Asp 180 185 190	635
gcc ata agc gat tta gcc tat ctt tgt tct aat gag ggg gcg ttt gag Ala Ile Ser Asp Leu Ala Tyr Leu Cys Ser Asn Glu Gly Ala Phe Glu 195 200 205	683
agc gat tat tta aac cct atc caa tca agc tat caa gct tta atg cga Ser Asp Tyr Leu Asn Pro Ile Gln Ser Ser Tyr Gln Ala Leu Met Arg 210 215 220	731
aaa gat agc cct aaa tta tac aac cat caa gcc acc aac cac tcg caa Lys Asp Ser Pro Lys Leu Tyr Asn His Gln Ala Thr Asn His Ser Gln 225 230 235 240	779
gcc gct tta gag aaa tta aaa ctc att aac aaa gaa caa ggc aaa gaa Ala Ala Leu Glu Lys Leu Lys Leu Ile Asn Lys Glu Gln Gly Lys Glu 245 250 255	827
tgc ttg cct aaa aac ttg cat ggc aaa cag caa ttc aaa agc aca tgg Cys Leu Pro Lys Asn Leu His Gly Lys Gln Gln Phe Lys Ser Thr Trp 260 265 270	875
ggg cgc ctg aat tgg aat aaa atc agc ccc acc ata gac aca cga ttt Gly Arg Leu Asn Trp Asn Lys Ile Ser Pro Thr Ile Asp Thr Arg Phe 275 280 285	923
gac act ccc agc aat ggc acc aac tcc cac ccc gaa ttg cac cgc tct Asp Thr Pro Ser Asn Gly Thr Asn Ser His Pro Glu Leu His Arg Ser 290 295 300	971

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atc acg cct aga gaa gcc gct agg ata caa agt ttt agc gat aat tat      1019
Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr
305                      310                      315                      320

atc ttt tat ggc aat aaa acg agc gtt tgt aag caa atc ggt aac gct      1067
Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala
                      325                      330                      335

gtg cct cct ctt cta gcc cta gcc tta ggc aaa gcg atc tta aaa agc      1115
Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys Ser
                      340                      345                      350

tta aga aaa tgatacaaat ttatcacgct gacgcttttg aaatcatcaa      1164
Leu Arg Lys
                      355

agactttttac cagcaaa      1181

<210> 240
<211> 355
<212> PRT
<213> Helicobacter pylori

<400> 240
Met Asn Tyr Lys Ile Leu Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser
 1          5          10          15
Ala Gly Leu Glu Cys Leu Glu Glu Phe Asp Ala Leu Ile Gly Leu Asp
20          25          30
Cys Asp Lys Gln Ala Leu Ile Thr Phe Glu Asn Asn His Lys Asn Ala
35          40          45
Ile Gly Val Cys Gly Asp Ile Thr Gln Thr Glu Ile Lys Glu Lys Val
50          55          60
Ile Lys Leu Ala Lys Lys Leu Glu Ile Asn Met Ile Ile Gly Gly Pro
65          70          75          80
Pro Cys Gln Gly Phe Ser Asn Lys Gly Lys Asn Leu Gly Leu Lys Asp
85          90          95
Pro Arg Asn Phe Leu Phe Leu Glu Tyr Ile Glu Ile Val Lys Ala Ile
100         105         110
Lys Pro Glu Ile Phe Ile Ile Glu Asn Val Lys Asn Leu Ile Ser Cys
115         120         125
Ala Lys Gly Tyr Phe Leu Glu Glu Ile Lys Glu Arg Leu Asn Ala Leu
130         135         140
Gly Tyr Gln Leu Ser Tyr Gln Ile Leu Asn Ala Lys Asp Tyr Gly Val
145         150         155         160
Pro Gln Asn Arg Glu Arg Ala Phe Ile Val Gly Ala Ser Arg Phe Ser
165         170         175
Phe Asp Phe Asn Leu Leu Glu Pro Ser Gln Ser Val Asn Val Gln Asp
180         185         190
Ala Ile Ser Asp Leu Ala Tyr Leu Cys Ser Asn Glu Gly Ala Phe Glu
195         200         205
Ser Asp Tyr Leu Asn Pro Ile Gln Ser Ser Tyr Gln Ala Leu Met Arg
210         215         220
Lys Asp Ser Pro Lys Leu Tyr Asn His Gln Ala Thr Asn His Ser Gln
225         230         235         240
Ala Ala Leu Glu Lys Leu Lys Leu Ile Asn Lys Glu Gln Gly Lys Glu
245         250         255
Cys Leu Pro Lys Asn Leu His Gly Lys Gln Gln Phe Lys Ser Thr Trp
260         265         270

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Gly Arg Leu Asn Trp Asn Lys Ile Ser Pro Thr Ile Asp Thr Arg Phe
 275 280 285
 Asp Thr Pro Ser Asn Gly Thr Asn Ser His Pro Glu Leu His Arg Ser
 290 295 300
 Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr
 305 310 315 320
 Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala
 325 330 335
 Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys Ser
 340 345 350
 Leu Arg Lys
 355

<210> 241
 <211> 1361
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (49)...(1305)

<400> 241

tattgatagc atgagttggt tttgggtttgg aattttaagg agtagctt atg aaa gag	57
Met Lys Glu	
1	
caa tca atg att gat ttt tta aaa ctt aga gat tat gac att aga aaa	105
Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp Ile Arg Lys	
5 10 15	
aca caa aat gcg cga tgg ata gat caa aaa tgc acc cct gat gtg ttg	153
Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro Asp Val Leu	
20 25 30 35	
tct ctt gtt gct gat tgt att tta gag ttt acg caa tgt aat att gga	201
Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys Asn Ile Gly	
40 45 50	
aaa tca ttt tct att agg gat att tgg gat agc cct tac acc aat gaa	249
Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr Thr Asn Glu	
55 60 65	
aat gtt aaa atg att ttt tct aaa cct gat tta aat tct gac ttt tcc	297
Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser Asp Phe Ser	
70 75 80	
atg cat gaa tac gat aag ttt ttt tct cag cct att aaa tta tta gcc	345
Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys Leu Leu Ala	
85 90 95	
tat agc ggt att tta ttt gaa aca aaa act ggc aat aga aat att tat	393
Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg Asn Ile Tyr	
100 105 110 115	
acc ata caa aac ata gag cta tta gaa tat ctc atg caa aga gaa aca	441
Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln Arg Glu Thr	
120 125 130	

aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta 1209
 Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val
 375 380 385

ata gat gct ttt tat ttt gat ttt aac aag agc aaa gat cca agt tgg 1257
 Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp
 390 395 400

tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt 1305
 Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe
 405 410 415

taataagttt tattgaaact ggctataaaa acccgcttga cttatcttat cctttt 1361

<210> 242
 <211> 419
 <212> PRT
 <213> Helicobacter pylori

<400> 242
 Met Lys Glu Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp
 1 5 10 15
 Ile Arg Lys Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro
 20 25 30
 Asp Val Leu Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys
 35 40 45
 Asn Ile Gly Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr
 50 55 60
 Thr Asn Glu Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser
 65 70 75 80
 Asp Phe Ser Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys
 85 90 95
 Leu Leu Ala Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg
 100 105 110
 Asn Ile Tyr Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln
 115 120 125
 Arg Glu Thr Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val
 130 135 140
 Leu Met Asp Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys
 145 150 155 160
 Gln Asp Thr Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe
 165 170 175
 Thr Ile Asn Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile
 180 185 190
 Phe Thr Lys Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly
 195 200 205
 Thr Arg Lys Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu
 210 215 220
 Asn Tyr Asn Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr
 225 230 235 240
 Thr Arg Gln Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser
 245 250 255
 Asn Tyr Leu Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp
 260 265 270
 Arg Phe Asn Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser
 275 280 285
 Gln Ala Thr Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile
 290 295 300

Ile Ala Asn Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His
 305 310 315 320
 Phe Ile Tyr Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp
 325 330 335
 Phe Gln Tyr Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp
 340 345 350
 Thr Gln Gly Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met
 355 360 365
 Gly Leu Lys Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu
 370 375 380
 Leu Lys Val Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp
 385 390 395 400
 Pro Ser Trp Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys
 405 410 415
 Leu Lys Phe

<210> 243
 <211> 2610
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (90)...(2558)

<400> 243
 taaagaggct tttgaaacca tgcttaaaga aattgagagc ttgaaacatt aatgcttcaa 60
 atgaatttgg tttaatcctt aatcccctt atg ctc ttt gat caa acc tta acc 113
 Met Leu Phe Asp Gln Thr Leu Thr
 1 5
 tat att tct tta ttt tct ggg gca gga gtg ggg tgc tat ggg ctt tta 161
 Tyr Ile Ser Leu Phe Ser Gly Ala Gly Val Gly Cys Tyr Gly Leu Leu
 10 15 20
 gaa gag ggg ttt gaa tgc gtt gct acc aat gaa att tta gaa aaa cgc 209
 Glu Glu Gly Phe Glu Cys Val Ala Thr Asn Glu Ile Leu Glu Lys Arg
 25 30 35 40
 ttg aat atc caa agg att aat cgc aaa tgc aaa tta gat gaa agc tac 257
 Leu Asn Ile Gln Arg Ile Asn Arg Lys Cys Lys Leu Asp Glu Ser Tyr
 45 50 55
 att agt ggg gac att aaa aag cca gaa aca aaa gaa aaa att tta aag 305
 Ile Ser Gly Asp Ile Lys Lys Pro Glu Thr Lys Glu Lys Ile Leu Lys
 60 65 70
 caa att gaa ttt tat tct aaa aaa ttt ggt aat gat agg gtt gat tta 353
 Gln Ile Glu Phe Tyr Ser Lys Lys Phe Gly Asn Asp Arg Val Asp Leu
 75 80 85
 gtg gta gca acc cca cct tgt caa ggc atg agc gta gcc aat cat aag 401
 Val Val Ala Thr Pro Pro Cys Gln Gly Met Ser Val Ala Asn His Lys
 90 95 100
 aag aaa aac gat gag atc aaa cgg aat tct ttg gtg gtt gaa agc att 449
 Lys Lys Asn Asp Glu Ile Lys Arg Asn Ser Leu Val Val Glu Ser Ile
 105 110 115 120

gat ttg atc aaa caa atc aaa ccc aga ttt ttt att tta gaa aat gtc Asp Leu Ile Lys Gln Ile Lys Pro Arg Phe Phe Ile Leu Glu Asn Val 125 130 135	497
cct agt ttt tat aaa aca ggt tgt ata gac aaa aat gat aat ttg cta Pro Ser Phe Tyr Lys Thr Gly Cys Ile Asp Lys Asn Asp Asn Leu Leu 140 145 150	545
gaa ata gga tct atg ata gag caa aat ttg agt ggc gat tat atg ctc Glu Ile Gly Ser Met Ile Glu Gln Asn Leu Ser Gly Asp Tyr Met Leu 155 160 165	593
tat gat gag gta atc aat ttt aaa aat ttt gga gct aat tca agc cga Tyr Asp Glu Val Ile Asn Phe Lys Asn Phe Gly Ala Asn Ser Ser Arg 170 175 180	641
aca aga act tta gtg ata ggg gtt tgt aaa gag ttt aaa gat ttt ata Thr Arg Thr Leu Val Ile Gly Val Cys Lys Glu Phe Lys Asp Phe Ile 185 190 195 200	689
agc gcg tta gaa ttt ttt cct gat ttc aaa caa gaa aaa acc tta aaa Ser Ala Leu Glu Phe Phe Pro Asp Phe Lys Gln Glu Lys Thr Leu Lys 205 210 215	737
gaa gtg ata gga tcg tta aaa cca ctt gct tgg ggc gag tat gac aac Glu Val Ile Gly Ser Leu Lys Pro Leu Ala Trp Gly Glu Tyr Asp Asn 220 225 230	785
acg gat ttt tat cat agt ttt aga act tat cca aag cat atg caa gaa Thr Asp Phe Tyr His Ser Phe Arg Thr Tyr Pro Lys His Met Gln Glu 235 240 245	833
tgg att aag gat tta aaa gaa gga caa agc gcg ttt gag aat aca gaa Trp Ile Lys Asp Leu Lys Glu Gly Gln Ser Ala Phe Glu Asn Thr Glu 250 255 260	881
tta aac aaa aaa cct cat aga att gtt ggc agt aag att gtc tta aat Leu Asn Lys Lys Pro His Arg Ile Val Gly Ser Lys Ile Val Leu Asn 265 270 275 280	929
gtt tct aaa aat ggc gat aaa tat aaa aga caa aaa tat cat agc gtt Val Ser Lys Asn Gly Asp Lys Tyr Lys Arg Gln Lys Tyr His Ser Val 285 290 295	977
gcc cct tgc att cat aca aga aac gac caa atg gct agc caa aac acg Ala Pro Cys Ile His Thr Arg Asn Asp Gln Met Ala Ser Gln Asn Thr 300 305 310	1025
atc cac ccc aaa gat gat aga gtg ttt tcc att aga gag ctg atg ctt Ile His Pro Lys Asp Asp Arg Val Phe Ser Ile Arg Glu Leu Met Leu 315 320 325	1073
tta atg aat atc cct agc cgt ttt aag tgg tta gat tta gaa tta caa Leu Met Asn Ile Pro Ser Arg Phe Lys Trp Leu Asp Leu Glu Leu Gln 330 335 340	1121
gaa tta aac gcc ctt aac caa caa gaa aaa gaa aaa atc tcc aaa caa Glu Leu Asn Ala Leu Asn Gln Gln Glu Lys Glu Lys Ile Ser Lys Gln 1169	1169

				405					410					415		
Phe	Ile	Leu	Glu	Asn	Gln	Asn	Lys	Ile	Ala	Arg	Ala	Ser	Leu	Val	Ser	
			420					425					430			
Leu	Ala	Glu	Met	Ser	Asn	Ser	Lys	Arg	Ile	Glu	Lys	Ser	Ala	Tyr	Phe	
		435					440					445				
Thr	Asn	Pro	Phe	Ile	Ile	Asn	Glu	Ile	Ala	Lys	Leu	Leu	Pro	Ser	Phe	
		450				455					460					
Lys	Gln	Glu	Ser	Val	Thr	Ile	Ile	Glu	Pro	Ser	Ala	Gly	Cys	Gly	Asn	
465					470					475					480	
Phe	Leu	Ser	Ala	Leu	Phe	Lys	Lys	Tyr	Thr	Ser	Val	Lys	Lys	Val	Tyr	
				485					490						495	
Leu	Lys	Cys	Ile	Asp	Ile	Asp	Lys	Asn	Ser	Leu	Glu	Ile	Leu	Glu	Ile	
			500					505					510			
Leu	Tyr	Lys	Asp	Cys	Ile	Pro	Asn	Asn	Phe	Glu	Met	Glu	Leu	Ile	Cys	
		515					520					525				
Lys	Asp	Phe	Leu	Ala	Tyr	Glu	Cys	Gly	Lys	Val	Asp	Leu	Ile	Val	Gly	
		530				535					540					
Asn	Pro	Pro	Phe	Gly	Lys	Thr	His	Glu	Arg	Phe	Lys	Asp	Tyr	Ser	Leu	
545					550					555					560	
Arg	Leu	Thr	His	Leu	Ala	Gly	Ile	Phe	Leu	Glu	Lys	Ser	Leu	Lys	Leu	
				565					570						575	
Ala	Asn	Phe	Thr	Ala	Met	Val	Met	Pro	Lys	Asn	Leu	Leu	Asn	Thr	Lys	
			580					585					590			
Glu	Tyr	Ala	Glu	Thr	Arg	Thr	Lys	Leu	Glu	Lys	Lys	Gly	Val	Gly	Ala	
		595					600					605				
Ile	Leu	Asp	Phe	Gly	Glu	Leu	Gly	Phe	Lys	Gly	Val	Leu	Val	Glu	Thr	
		610				615					620					
Ile	Ala	Ile	Val	Thr	Gln	Lys	Ser	Lys	Glu	Val	Leu	Ala	Arg	Ser	Leu	
625					630					635					640	
Pro	Leu	Asn	Leu	Ser	Ile	Lys	Gln	Lys	Pro	Ser	Tyr	Ile	Phe	Asp	Lys	
				645					650					655		
Gln	Leu	Pro	Tyr	Trp	Val	Ile	Tyr	Arg	Asn	Ala	Phe	Phe	Asp	Lys	Val	
			660					665					670			
Phe	His	Ser	Met	Gln	Phe	Gly	Leu	Phe	Glu	Val	Phe	Arg	Asp	Arg	Gln	
		675					680					685				
Ile	Thr	Asn	Ser	Val	Leu	Val	Lys	Asn	Gly	Ile	Arg	Val	Ile	Lys	Ser	
		690				695					700					
Arg	Asn	Ile	Asp	Glu	Asn	Gly	Lys	Ile	Ile	Ser	Ile	Glu	Asn	Tyr	Asp	
705					710					715					720	
Ser	Tyr	Ile	Gln	Lys	Glu	Val	Leu	Ser	Pro	Phe	Lys	Ile	Ala	Ser	Phe	
				725					730					735</		

-279-

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 <222> (54)...(3608)

<400> 245

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                                     Met
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caa aaa atc att gac gat tcg cta gaa tta gct aaa aaa ctg caa gat      104
Gln Lys Ile Ile Asp Asp Ser Leu Glu Leu Ala Lys Lys Leu Gln Asp
          5                      10                      15

agt atc agt aac cat ttg agc gat cag gaa aaa gcg ttc cac tct aaa      152
Ser Ile Ser Asn His Leu Ser Asp Gln Glu Lys Ala Phe His Ser Lys
          20                      25                      30

atg caa aag ctt tta aac aac cct gaa aac aaa gtc atg ctc ata gag      200
Met Gln Lys Leu Leu Asn Asn Pro Glu Asn Lys Val Met Leu Ile Glu
          35                      40                      45

ctt atg gat cgg agt ttc agg tgc ttg gac aat aaa gcc cgc ttt gaa      248
Leu Met Asp Arg Ser Phe Arg Cys Leu Asp Asn Lys Ala Arg Phe Glu
          50                      55                      60                      65

atg att gag cat gtt tta gac aaa tac aaa agc cgt gag att ttt tct      296
Met Ile Glu His Val Leu Asp Lys Tyr Lys Ser Arg Glu Ile Phe Ser
          70                      75                      80

ccg ttt gaa aaa gtg ctt tta atg ggg ttt tta agc ttt ggg aaa atg      344
Pro Phe Glu Lys Val Leu Leu Met Gly Phe Leu Ser Phe Gly Lys Met
          85                      90                      95

ctc cct gat atg agc gtg cct ttc ttt gtc aat aaa atc aga agc gac      392
Leu Pro Asp Met Ser Val Pro Phe Phe Val Asn Lys Ile Arg Ser Asp
          100                      105                      110

acg aaa gcg atg gtc ttg gat caa gaa gag agc cag tta aaa gag cgg      440
Thr Lys Ala Met Val Leu Asp Gln Glu Glu Ser Gln Leu Lys Glu Arg
          115                      120                      125

att tta aaa aga aaa aat gaa aaa atc att ttg aat gtg aat ttt att      488
Ile Leu Lys Arg Lys Asn Glu Lys Ile Ile Leu Asn Val Asn Phe Ile
          130                      135                      140                      145

ggc gaa gag gtt tta ggc gaa gaa gaa gct aat gcg cgt ttt gaa aaa      536
Gly Glu Glu Val Leu Gly Glu Glu Glu Ala Asn Ala Arg Phe Glu Lys
          150                      155                      160

tac tct caa gcc cta aaa tcc aac tac atc caa tac att tcc att aaa      584
Tyr Ser Gln Ala Leu Lys Ser Asn Tyr Ile Gln Tyr Ile Ser Ile Lys
          165                      170                      175

atc acg acg att ttt tct caa atc aat atc ctt gat ttt gaa tac tct      632
Ile Thr Thr Ile Phe Ser Gln Ile Asn Ile Leu Asp Phe Glu Tyr Ser
          180                      185                      190

aaa aaa gag att gtc aaa cgc cta gac gct ctt tac gcc ctg gct tta      680
Lys Lys Glu Ile Val Lys Arg Leu Asp Ala Leu Tyr Ala Leu Ala Leu

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Trp	Lys	Asp	Gln	Glu	Gln	Arg	Phe	Leu	Asn	Ser	Leu	Lys	Gly	Ile	Ala		
435						440					445						
act	tta	gac	aat	gcc	acc	cat	agg	act	caa	gat	agg	aac	gcc	aaa	caa		1448
Thr	Leu	Asp	Asn	Ala	Thr	His	Arg	Thr	Gln	Asp	Arg	Asn	Ala	Lys	Gln		
450					455					460					465		
agc	ggg	cat	acc	act	tac	cca	aac	cac	tcc	ttt	aaa	aac	gaa	agc	gat		1496
Ser	Gly	His	Thr	Thr	Tyr	Pro	Asn	His	Ser	Phe	Lys	Asn	Glu	Ser	Asp		
				470					475						480		
acc	gat	ttt	att	tta	aaa	gcc	aac	cga	gaa	tgg	gct	aaa	aaa	gtg	cgc		1544
Thr	Asp	Phe	Ile	Leu	Lys	Ala	Asn	Arg	Glu	Trp	Ala	Lys	Lys	Val	Arg		
			485					490						495			
gag	aaa	atg	cgt	aac	gct	cct	att	tta	gag	ctt	tac	cca	gag	atg	gat		1592
Glu	Lys	Met	Arg	Asn	Ala	Pro	Ile	Leu	Glu	Leu	Tyr	Pro	Glu	Met	Asp		
		500					505					510					
ggg	agg	ttt	gaa	gat	cct	aat	cta	acc	cct	tta	gaa	gtc	ttt	gat	aga		1640
Gly	Arg	Phe	Glu	Asp	Pro	Asn	Leu	Thr	Pro	Leu	Glu	Val	Phe	Asp	Arg		
	515					520					525						
atc	cat	cat	aaa	aaa	atc	gct	agc	gtg	cat	tta	gcg	gat	aag	gaa	gcg		1688
Ile	His	His	Lys	Lys	Ile	Ala	Ser	Val	His	Leu	Ala	Asp	Lys	Glu	Ala		
530					535					540					545		
att	tta	aaa	gcc	cta	gaa	gtg	gct	aaa	agc	gat	aag	agc	cgt	ttc	agt		1736
Ile	Leu	Lys	Ala	Leu	Glu	Val	Ala	Lys	Ser	Asp	Lys	Ser	Arg	Phe	Ser		
				550					555						560		
caa	aaa	agc	ttt	aca	gaa	atc	cat	gcc	tta	atg	agt	caa	acc	gcc	cag		1784
Gln	Lys	Ser	Phe	Thr	Glu	Ile	His	Ala	Leu	Met	Ser	Gln	Thr	Ala	Gln		
			565					570						575			
ctt	ttt	aga	gaa	aga	aga	ggc	gat	ttg	ata	ggg	att	tcc	gct	tta	gaa		1832
Leu	Phe	Arg	Glu	Arg	Arg	Gly	Asp	Leu	Ile	Gly	Ile	Ser	Ala	Leu	Glu		
		580					585					590					
gtg	ggt	aag	act	ttc	gct	gaa	acg	gac	gct	gaa	gtg	agc	gaa	gcc	att		1880
Val	Gly	Lys	Thr	Phe	Ala	Glu	Thr	Asp	Ala	Glu	Val	Ser	Glu	Ala	Ile		
		595				600					605						
gac	ttt	tta	gag	ttt	tac	cct	tac	agc	tta	agg	gtg	ttg	caa	gag	caa		1928
Asp	Phe	Leu	Glu	Phe	Tyr	Pro	Tyr	Ser	Leu	Arg	Val	Leu	Gln	Glu	Gln		
610					615					620					625		
aac	aca	aaa	acg	caa	ttc	acc	cct	aaa	ggc	gtg	ggc	gtg	gtc	att	gcc		1976
Asn	Thr	Lys	Thr	Gln	Phe	Thr	Pro	Lys	Gly	Val	Gly	Val	Val	Ile	Ala		
				630					635					640			
cca	tgg	aat	ttc	cct	gtg	ggc	att	tct	gta	ggc	act	atc	gct	gcc	ccc		2024
Pro	Trp	Asn	Phe	Pro	Val	Gly	Ile	Ser	Val	Gly	Thr	Ile	Ala	Ala	Pro		
			645					650						655			
cta	gct	acg	ggc	aat	cgg	gtg	att	tac	aag	ccc	tca	agt	ttg	tct	agc		2072
Leu	Ala	Thr	Gly	Asn	Arg	Val	Ile	Tyr	Lys	Pro	Ser	Ser	Leu	Ser	Ser		
			660				665					670					

Leu Ser Leu Ser Val Gly Asp Pro Phe Asp Phe Lys Asn Lys Ile Gly
 805 810 815
 Ala Leu Ala Asp Lys Pro Asn Glu Lys Val Ile Lys Ala Ile Asp Glu
 820 825 830
 Leu Lys Ser Tyr Glu Asn Tyr Glu Ile Pro Val Ser Phe Val Asn Asp
 835 840 845
 Asn Pro Tyr Leu Met Lys Pro Ser Ile Lys Tyr Gly Thr Lys Lys Gly
 850 855 860
 Asp Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met
 865 870 875 880
 Glu Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly
 885 890 895
 Tyr Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu
 900 905 910
 Tyr Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro
 915 920 925
 Thr Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys
 930 935 940
 Ser Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr
 945 950 955 960
 Gln Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys
 965 970 975
 Asn Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp
 980 985 990
 Glu His Thr His Glu Leu Lys Arg Ala Ile Phe Met Ala Lys Ser Tyr
 995 1000 1005
 Ala Tyr His Tyr Lys His Glu Phe Ser Gln Thr Lys Asp Tyr Val Lys
 1010 1015 1020
 Ile Arg Gly Glu Asp Asn Leu Phe Ser Tyr Thr Lys Val Lys Ser Val
 1025 1030 1035 104
 Gly Tyr Arg Ile Thr Glu Lys Asp Thr Leu Ser Asp Met Leu Gly Val
 1045 1050 1055
 Ala Leu Ala Cys Leu Ile Ser Gln Ile Pro Leu Thr Leu Ser Ile Glu
 1060 1065 1070
 Asn Glu Arg Thr Asn Lys Asp Leu Thr Phe Phe Leu Glu Cys Leu Lys
 1075 1080 1085
 Ala Leu Gln Ala Ser Ala Pro Ile Val Tyr Glu Ser Leu Gln Lys Phe
 1090 1095 1100
 Ser Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp
 1105 1110 1115 112
 Leu Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala
 1125 1130 1135
 Thr Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His
 1140 1145 1150
 Leu Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly
 1155 1160 1165
 Ser Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu
 1170 1175 1180
 Lys
 1185

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 <213> Helicobacter pylori

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 <222> (107)...(673)

<212> PRT
<213> Helicobacter pylori

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			20					25					30		
Gly	Phe	Val	Pro	Leu	Lys	Glu	Gly	Phe	Leu	Lys	Ser	Phe	Lys	Glu	Arg
		35					40					45			
Cys	Asn	Leu	Glu	Phe	Leu	Glu	Asn	Leu	Asp	Leu	Leu	Phe	Leu	Tyr	Asp
50						55					60				
Lys	Pro	Ser	Ala	His	Glu	Ile	Phe	Ser	Leu	Cys	Lys	Glu	Leu	Lys	Asn
65					70					75					80
Ser	Ile	Trp	Asp	Arg	Lys	Leu	Val	Val	Ala	Leu	Val	Glu	Ala	Leu	Glu
				85					90					95	
Gly	Phe	Lys	Asp	Trp	Asn	Leu	Ser	Leu	Lys	Ile	Glu	Asp	Lys	Arg	Ser
			100					105					110		
Asn	Ser	Leu	Gly	Asn	Gly	Thr	Lys	Lys	Leu	Leu	Thr	Asn	Ala	Asp	Leu
		115					120						125		
Gly	Ser	Asp	Tyr	Lys	Thr	Ile	Val	Ile	Asp	Ser	Met	Lys	Thr	Tyr	His
		130				135					140				
Gln	Ser	Gln	Gln	Glu	Lys	Tyr	Lys	Arg	Glu	Arg	Gly	Glu	Thr	Leu	Glu
145					150					155					160
Val	Arg	Pro	Thr	Thr	Pro	Pro	Ser	Tyr	Gly	Gly	Gly	Ser	Ile	Arg	Ile
				165					170					175	
Ser	Gly	Asp	Lys	Lys	Pro	Asp	Phe	Asp	Glu	Glu	Asn	Phe			
			180					185							

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<222> (58)...(852)

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Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile Gly	
5 10 15	
gct gat ggg cgg tgc gtg att gaa gac aat ttt ttc acg ccc ccc ttt	156
Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro Phe	
20 25 30	
aag ctc atg gcg ccc ttt tac cct aaa gac gat tta gcg gaa atc atg	204
Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile Met	
35 40 45	
ctt tta gcg gta agc cct ggc atg atg agg ggc gat gcg caa gat gtg	252
Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp Val	
50 55 60 65	

caa tta aac atc ggt cca aat tgc aag tta agg atc act tcg caa tcc Gln Leu Asn Ile Gly Pro Asn Cys Lys Leu Arg Ile Thr Ser Gln Ser 70 75 80	300
ttt gaa aaa atc cat aac act gaa gat ggg ttt gcc agc aga gac atg Phe Glu Lys Ile His Asn Thr Glu Asp Gly Phe Ala Ser Arg Asp Met 85 90 95	348
cat att gtt gtg ggg gaa aac gct ttt tta gat ttt gcg cct ttc ccg His Ile Val Val Gly Glu Asn Ala Phe Leu Asp Phe Ala Pro Phe Pro 100 105 110	396
tta atc ccc ttt gaa aac gcg cat ttt aag ggc aac acc acg att tct Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile Ser 115 120 125	444
ttg cgc tct agc tct caa ttg ctc tat agt gaa atc att gtc gca ggg Leu Arg Ser Ser Ser Gln Leu Leu Tyr Ser Glu Ile Ile Val Ala Gly 130 135 140 145	492
cga gtg gcg cgc aat gag ttg ttt aaa ttc aac cgc ttg cac acc aaa Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr Lys 150 155 160	540
atc tct att tta caa gat gag aaa ccc atc tat tat gac aac acg att Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile 165 170 175	588
tta gat ccc aaa acc acc gac tta aat aac atg tgc atg ttt gat ggc Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp Gly 180 185 190	636
tat acg cat tat ttg aat ttg gtg ctt gtc aat tgc ccc ata gag ctc Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu Leu 195 200 205	684
tct ggt gtg cga gaa tgc att gaa gaa agc gaa ggg gtg gat ggg gca Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu Gly Val Asp Gly Ala 210 215 220 225	732
gtg agt gaa acc gct agt tct cat tta tgc gtg aaa gct tta gcg aaa Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala Lys 230 235 240	780
ggc tca gaa ccc tta ttg cat tta aga gaa aaa atc gct cgc ttg gtt Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu Val 245 250 255	828
acg caa acc acc acg caa aag gtt tgaaagcact tcaaaaagat taaagtcctt Thr Gln Thr Thr Thr Gln Lys Val 260 265	882
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 <212> PRT
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ggt gaa cac aac att ctt ccc gct tcc act aac ccc act atc cct ttc Gly Glu His Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile Pro Phe 295 300 305	968
act gtg aat aca gaa gca gaa cac atg gac atg ctt atg gtg tgc cac Thr Val Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val Cys His 310 315 320	1016
cac ttg gat aaa agc att aaa gaa gat gtt cag ttc gct gat tca agg His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp Ser Arg 325 330 335	1064
atc cgc cct caa acc att gcg gct gaa gac act ttg cat gac atg ggg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Thr Leu His Asp Met Gly 340 345 350	1112
att ttc tca atc acc agc tct gac tct caa gct atg ggt cgt gtg ggt Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Val Gly 355 360 365 370	1160
gaa gtt atc act aga act tgg caa aca gct gac aaa aac aaa aaa gaa Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu 375 380 385	1208
ttt ggc cgc ttg aaa gaa gaa aaa ggc gat aac gac aac ttc agg atc Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe Arg Ile 390 395 400	1256
aaa cgc tac ttg tct aaa tac acc att aac cca gcg atc gct cat ggg Lys Arg Tyr Leu Ser Lys Tyr Thr Ile Asn Pro Ala Ile Ala His Gly 405 410 415	1304
att agc gag tat gta ggt tct gta gaa gtg ggc aaa gtg gct gac ttg Ile Ser Glu Tyr Val Gly Ser Val Glu Val Gly Lys Val Ala Asp Leu 420 425 430	1352
gta ttg tgg agt ccc gca ttc ttt ggc gta aaa ccc aac atg atc atc Val Leu Trp Ser Pro Ala Phe Phe Gly Val Lys Pro Asn Met Ile Ile 435 440 445 450	1400
aaa ggc ggg ttc att gcg ttg agt caa atg ggt gac gcg aac gct tct Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn Ala Ser 455 460 465	1448
atc cct acc cca caa cca gtt tat tac aga gaa atg ttc gct cat cat Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala His His 470 475 480	1496
ggt aaa gcc aaa tac gat gca aac atc act ttt gtg tct caa gcg gct Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln Ala Ala 485 490 495	1544
tat gac aaa ggc att aaa gaa gaa tta ggg ctt gaa aga caa gtg ttg Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln Val Leu 500 505 510	1592

ccg gta aaa aat tgc aga aac atc act aaa aaa gac atg caa ttc aac 1640
 Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln Phe Asn
 515 520 525 530

gac act acc gct cac att gaa gtc aat cct gaa act tac cat gtg ttc 1688
 Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His Val Phe
 535 540 545

gtg gat ggc aaa gaa gta act tct aaa cca gcc aat aaa gtg agc ttg 1736
 Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val Ser Leu
 550 555 560

gcg caa ctc ttt agc att ttc taggattttt taggagcaac gctccttaaa 1787
 Ala Gln Leu Phe Ser Ile Phe
 565

tccttagttt ttagctctct gatttttt 1815

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 Glu His Asp Tyr Thr Ile Tyr Gly Glu Glu Leu Lys Phe Gly Gly Gly
 35 40 45
 Lys Thr Leu Arg Glu Gly Met Ser Gln Ser Asn Asn Pro Ser Lys Glu
 50 55 60
 Glu Leu Asp Leu Ile Ile Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly
 65 70 75 80
 Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile
 85 90 95
 Gly Lys Gly Gly Asn Lys Asp Met Gln Asp Gly Val Lys Asn Asn Leu
 100 105 110
 Ser Val Gly Pro Ala Thr Glu Ala Leu Ala Gly Glu Gly Leu Ile Val
 115 120 125
 Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln
 130 135 140
 Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly
 145 150 155 160
 Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg
 165 170 175
 Arg Asn Leu Lys Trp Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn
 180 185 190
 Leu Gly Phe Leu Ala Lys Gly Asn Ala Ser Asn Asp Ala Ser Leu Ala
 195 200 205
 Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp
 210 215 220
 Gly Thr Thr Pro Ser Ala Ile Asn His Ala Leu Asp Val Ala Asp Lys
 225 230 235 240
 Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly
 245 250 255
 Cys Val Glu Asp Thr Met Ala Ala Ile Ala Gly Arg Thr Met His Thr
 260 265 270

Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys Tyr Asn Ala
 100 105 110

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 Met Ala
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 Lys Glu Asn Pro Pro Ile Val Phe Gly Pro Val Leu Ser Arg Arg Phe
 5 10 15

ggg aag tct ttg ggc gtg gat cta tcg ccc tct aaa aaa caa tgc aat 152
 Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln Cys Asn
 20 25 30

tac aat tgc att tat tgc gag ttg ggt aaa gcc aag ccc att gaa cgc 200
 Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile Glu Arg
 35 40 45 50

atg gaa gaa gtg atc aaa gtg gaa acc ttg att aac gcc att caa aac 248
 Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile Gln Asn
 55 60 65

gcc cta aac aac ctc acc acc ccc att gat gtt tta acc att acc gct 296
 Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile Thr Ala
 70 75 80

aat ggc gaa ccc acg cta tac cct cat tta tta gag ctt atc caa agc 344
 Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile Gln Ser
 85 90 95

atc aag cct ttt tta aag ggc gtt aaa act ttg att tta agc aat ggc 392
 Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser Asn Gly
 100 105 110

tcg ctc ttt tat gag cca aaa gtc cag caa gcc tta aag gaa ttt gac 440
 Ser Leu Phe Tyr Glu Pro Lys Val Gln Gln Ala Leu Lys Glu Phe Asp
 115 120 125 130

atc gtt aaa ttt tct tta gac gct att gat ttg aaa gcc ttt gaa aga 488
 Ile Val Lys Phe Ser Leu Asp Ala Ile Asp Leu Lys Ala Phe Glu Arg
 135 140 145

gtg gat aaa ccc tat tct aaa gac att aat aag att tta gag ggg att 536
 Val Asp Lys Pro Tyr Ser Lys Asp Ile Asn Lys Ile Leu Glu Gly Ile
 150 155 160

ttg cgc ttt tct caa att tat caa ggg caa ttg gtg gct gaa gtg ttg 584
 Leu Arg Phe Ser Gln Ile Tyr Gln Gly Gln Leu Val Ala Glu Val Leu

165	170	175	
tta att aag ggc gtg aat gat agc gcg aac aac tta aaa ctc atc gct Leu Ile Lys Gly Val Asn Asp Ser Ala Asn Asn Leu Lys Leu Ile Ala 180 185 190			632
gcc ttt tta aaa caa atc aat ata gcc aga gtg gat tta agc acc ata Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser Thr Ile 195 200 205 210			680
gac aga ccc tca agc ttt aaa gcc cct aaa tta agc gaa gat gaa ttg Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp Glu Leu 215 220 225			728
tta aaa tgc tct tta ttt ttt gaa ggg ctt tgc gtg agt ttg cct aaa Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu Pro Lys 230 235 240			776
cga tcc att act caa gct aaa aaa ttg att tct tgc ggt ata gac gaa Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile Asp Glu 245 250 255			824
ttg ctc gct tta att tcc agg cgc cct tta agc gca gaa gaa gcc ccc Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu Ala Pro 260 265 270			872
cta att cta gat tct aac gct ttt aag cat tta gaa act ttg tta aac Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu Leu Asn 275 280 285 290			920
cat aag caa att acg att aaa aaa gtc ggc tct ttg gag ttt tat tgc His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe Tyr Cys 295 300 305			968
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aaa			1027
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Arg Phe Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln 20 25 30			
Cys Asn Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile 35 40 45			
Glu Arg Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile 50 55 60			
Gln Asn Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile 65 70 75 80			
Thr Ala Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile 85 90 95			
Gln Ser Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser			

Asn	Gly	Ser	Leu	Phe	Tyr	Glu	Pro	Lys	Val	Gln	Gln	Ala	Leu	Lys	Glu
	115						120					125			
Phe	Asp	Ile	Val	Lys	Phe	Ser	Leu	Asp	Ala	Ile	Asp	Leu	Lys	Ala	Phe
	130						135				140				
Glu	Arg	Val	Asp	Lys	Pro	Tyr	Ser	Lys	Asp	Ile	Asn	Lys	Ile	Leu	Glu
	145				150					155					160
Gly	Ile	Leu	Arg	Phe	Ser	Gln	Ile	Tyr	Gln	Gly	Gln	Leu	Val	Ala	Glu
				165					170					175	
Val	Leu	Leu	Ile	Lys	Gly	Val	Asn	Asp	Ser	Ala	Asn	Asn	Leu	Lys	Leu
			180					185					190		
Ile	Ala	Ala	Phe	Leu	Lys	Gln	Ile	Asn	Ile	Ala	Arg	Val	Asp	Leu	Ser
	195						200					205			
Thr	Ile	Asp	Arg	Pro	Ser	Ser	Phe	Lys	Ala	Pro	Lys	Leu	Ser	Glu	Asp
	210				215						220				
Glu	Leu	Leu	Lys	Cys	Ser	Leu	Phe	Phe	Glu	Gly	Leu	Cys	Val	Ser	Leu
	225				230					235					240
Pro	Lys	Arg	Ser	Ile	Thr	Gln	Ala	Lys	Lys	Leu	Ile	Ser	Cys	Gly	Ile
			245						250					255	
Asp	Glu	Leu	Leu	Ala	Leu	Ile	Ser	Arg	Arg	Pro	Leu	Ser	Ala	Glu	Glu
		260						265					270		
Ala	Pro	Leu	Ile	Leu	Asp	Ser	Asn	Ala	Phe	Lys	His	Leu	Glu	Thr	Leu
	275						280					285			
Leu	Asn	His	Lys	Gln	Ile	Thr	Ile	Lys	Lys	Val	Gly	Ser	Leu	Glu	Phe
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Tyr	Cys	Ala	Phe												
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Met Glu Ser Val Lys Thr Gly Lys Thr	
1 5	
aat aag gtt ggc aag aat aca gag atg gct aat aca aag gca aat aaa	161
Asn Lys Val Gly Lys Asn Thr Glu Met Ala Asn Thr Lys Ala Asn Lys	
10 15 20 25	
gag act cat ttt aaa caa gtg agc gcc att aca aat ata atc aga tca	209
Glu Thr His Phe Lys Gln Val Ser Ala Ile Thr Asn Ile Ile Arg Ser	
30 35 40	
gtt ggt ggg ttt ttt aca aaa att gca aag aga gtt aga gga ctt gta	257
Val Gly Gly Phe Phe Thr Lys Ile Ala Lys Arg Val Arg Gly Leu Val	
45 50 55	
aaa aaa cac ccc aag aaa agc agt gcg gca tta gta gta ttg acc cat	305
Lys Lys His Pro Lys Lys Ser Ser Ala Ala Leu Val Val Leu Thr His	
60 65 70	

att gcg tgc aag aaa gcg aaa gaa tta gac gat aaa gtc caa gat aaa Ile Ala Cys Lys Lys Ala Lys Glu Leu Asp Asp Lys Val Gln Asp Lys 75 80 85	353
tcc aaa caa gct gaa aaa gaa aat caa atc aat tgg tgg aaa tat tca Ser Lys Gln Ala Glu Lys Glu Asn Gln Ile Asn Trp Trp Lys Tyr Ser 90 95 100 105	401
gga tta aca ata gcg gca agt tta tta tta gcc gct tgt agc gct ggt Gly Leu Thr Ile Ala Ala Ser Leu Leu Leu Ala Ala Cys Ser Ala Gly 110 115 120	449
gat act gat aaa cag ata gaa cta gaa caa gaa aaa aag gaa gct gaa Asp Thr Asp Lys Gln Ile Glu Leu Glu Gln Glu Lys Lys Glu Ala Glu 125 130 135	497
aac gct agg gat aga gcg aac aag agt ggg ata gaa cta gaa caa gaa Asn Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu 140 145 150	545
aga cag aaa aca aac aag agt ggg ata gaa ctc gct aat agt caa ata Arg Gln Lys Thr Asn Lys Ser Gly Ile Glu Leu Ala Asn Ser Gln Ile 155 160 165	593
aaa gca gaa caa gaa aga caa aag aca gaa caa gaa aaa caa aaa gca Lys Ala Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys Ala 170 175 180 185	641
aat aag agt gcg ata gag tta gaa cag caa aaa caa aag acc att aat Asn Lys Ser Ala Ile Glu Leu Glu Gln Gln Lys Gln Lys Thr Ile Asn 190 195 200	689
aca caa aga gat ttg att aaa gaa cag aaa gat ttc att aaa gaa aca Thr Gln Arg Asp Leu Ile Lys Glu Gln Lys Asp Phe Ile Lys Glu Thr 205 210 215	737
gaa caa aat tgc caa gaa aat cat aat caa ttc ttt att aaa aaa tta Glu Gln Asn Cys Gln Glu Asn His Asn Gln Phe Phe Ile Lys Lys Leu 220 225 230	785
gga att aag ggt ggc att gct ata gaa gta gaa gct gaa tgc aaa acc Gly Ile Lys Gly Gly Ile Ala Ile Glu Val Glu Ala Glu Cys Lys Thr 235 240 245	833
cct aaa cct gca aaa acc aat caa acc cct atc cag cca aaa cac ctc Pro Lys Pro Ala Lys Thr Asn Gln Thr Pro Ile Gln Pro Lys His Leu 250 255 260 265	881
cca aac tct aaa caa cct cat tct caa aga gga tca aaa gcg caa gag Pro Asn Ser Lys Gln Pro His Ser Gln Arg Gly Ser Lys Ala Gln Glu 270 275 280	929
ttt atc gct tat ttg caa aaa gag cta gaa ttt ctg ccc tat tcg caa Phe Ile Ala Tyr Leu Gln Lys Glu Leu Phe Leu Pro Tyr Ser Gln 285 290 295	977
aaa gct atc gct aaa caa gtg aat ttc tat aaa cca agt tct atc gct Lys Ala Ile Ala Lys Gln Val Asn Phe Tyr Lys Pro Ser Ser Ile Ala 300 305 310	1025

agc tac aga gat ttg ccc tta agg ttt tat gaa tac ggc gtg gtg cat	1064
Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val Val His	
325 330 335	
cgg cat gaa aaa agc ggc gtg ttg cat ggg ctt tta agg gtt agg gaa	1112
Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val Arg Glu	
340 345 350	
ttt acc caa gat gat gca cat att ttt tgc tct ttt gaa cag atc caa	1160
Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln Ile Gln	
355 360 365 370	
agc gaa gtg agc gcg att tta gat ttt acg cac aaa atc atg caa gcg	1208
Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met Gln Ala	
375 380 385	
ttt gat ttt agc tat gaa atg gaa tta tcc aca agg ccg gct aaa tcc	1256
Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala Lys Ser	
390 395 400	
ata ggc gat gat aaa gtt tgg gaa aag gcc act aac gct tta aaa gaa	1304
Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu Lys Glu	
405 410 415	
gcc tta aaa gaa cac cgc att gat tac aag att gat gaa ggg gga ggg	1352
Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly Gly Gly	
420 425 430	
gct ttc tat ggg cct aag att gac att aaa atc act gac gct tta aag	1400
Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala Leu Lys	
435 440 445 450	
cgt aaa tgg cag tgt ggc acg att caa gtg gat atg aat ttg cct gaa	1448
Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu Pro Glu	
455 460 465	
cgc ttc aag ctc gct ttc act aat gag tat aat cac gct gag cag ccg	1496
Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu Gln Pro	
470 475 480	
gtg atg atc cac aga gcg att tta ggc tcg ttt gaa agg ttt att gcg	1544
Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe Ile Ala	
485 490 495	
att ttg agc gaa cat ttt ggg ggg aat ttc cct ttc ttt gtc gcg ccc	1592
Ile Leu Ser Glu His Phe Gly Gly Asn Phe Pro Phe Phe Val Ala Pro	
500 505 510	
act caa atc gct ctc atc cct att aat gaa gag cat cat gtt ttt gct	1640
Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val Phe Ala	
515 520 525 530	
ttg aaa tta aaa gag gcg cta aaa aag cgc gat att ttt gta gaa gtg	1688
Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val Glu Val	
535 540 545	
tta gat aaa aac gac agc ttg aat aaa aag gtg cga tta gcc gaa aag	1736
Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala Glu Lys	

550	555	560	
caa aaa atc cct atg att tta gtg tta ggg aat gaa gaa gtg gag acc			1784
Gln Lys Ile Pro Met Ile Leu Val Leu Gly Asn Glu Glu Val Glu Thr			
565	570	575	
gaa att tta tcc att aga gac aga gaa aaa caa gat caa tat aaa atg			1832
Glu Ile Leu Ser Ile Arg Asp Arg Glu Lys Gln Asp Gln Tyr Lys Met			
580	585	590	
ccc tta aag gag ttt tta aac atg gtt gaa tct aag atg caa gag gtt			1880
Pro Leu Lys Glu Phe Leu Asn Met Val Glu Ser Lys Met Gln Glu Val			
595	600	605	610
agt ttt tgagtagaaa cgaagtgttg ttaaaccggag acattaattt taaagaagtg			1936
Ser Phe			
cgt			1939
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Leu Glu Ser Ala Lys Val Leu Gly Leu Ser Asp Gly Ile Lys Ala Leu			
20 25 30			
Asn Gly Thr Glu Pro Ile Tyr Phe Asp Asp Ser Pro Leu Ala Leu Glu			
35 40 45			
Val Ile Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala			
50 55 60			
Leu Tyr Pro Asp Ala Lys Phe Phe Val Gly Pro Val Val Glu Glu Gly			
65 70 75 80			
Phe Tyr Tyr Asp Phe Lys Thr Ser Ser Lys Ile Ser Glu Glu Asp Leu			
85 90 95			
Pro Lys Ile Glu Ala Lys Met Lys Glu Phe Ala Lys Leu Lys Leu Ala			
100 105 110			
Ile Thr Lys Glu Thr Leu Thr Arg Glu Gln Ala Leu Glu Arg Phe Lys			
115 120 125			
Gly Asp Glu Leu Lys His Ala Val Met Ser Lys Ile Gly Gly Asp Ala			
130 135 140			
Phe Gly Val Tyr Gln Gln Gly Glu Phe Glu Asp Leu Cys Lys Gly Pro			
145 150 155 160			
His Leu Pro Asn Thr Arg Phe Leu Asn His Phe Lys Leu Thr Lys Leu			
165 170 175			
Ala Gly Ala Tyr Leu Gly Gly Asp Glu Asn Asn Glu Met Leu Ile Arg			
180 185 190			
Ile Tyr Gly Ile Ala Phe Ala Thr Lys Glu Gly Leu Lys Asp Tyr Leu			
195 200 205			
Phe Gln Ile Glu Glu Ala Lys Lys Arg Asp His Arg Lys Leu Gly Val			
210 215 220			
Glu Leu Gly Leu Phe Ser Phe Asp Asp Glu Ile Gly Ala Gly Leu Pro			
225 230 235 240			
Leu Trp Leu Pro Lys Gly Ala Arg Leu Arg Lys Arg Ile Glu Asp Leu			
245 250 255			
Leu Ser Gln Ala Leu Leu Leu Arg Gly Tyr Glu Pro Val Lys Gly Pro			

			260					265					270			
Glu	Ile	Leu	Lys	Ser	Asp	Val	Trp	Lys	Ile	Ser	Gly	His	Tyr	Asp	Asn	
		275					280					285				
Tyr	Lys	Glu	Asn	Met	Tyr	Phe	Thr	Thr	Ile	Asp	Glu	Gln	Glu	Tyr	Gly	
	290					295					300					
Ile	Lys	Pro	Met	Asn	Cys	Val	Gly	His	Ile	Lys	Val	Tyr	Gln	Ser	Ala	
305					310					315					320	
Leu	His	Ser	Tyr	Arg	Asp	Leu	Pro	Leu	Arg	Phe	Tyr	Glu	Tyr	Gly	Val	
				325					330					335		
Val	His	Arg	His	Glu	Lys	Ser	Gly	Val	Leu	His	Gly	Leu	Leu	Arg	Val	
			340					345					350			
Arg	Glu	Phe	Thr	Gln	Asp	Asp	Ala	His	Ile	Phe	Cys	Ser	Phe	Glu	Gln	
		355					360					365				
Ile	Gln	Ser	Glu	Val	Ser	Ala	Ile	Leu	Asp	Phe	Thr	His	Lys	Ile	Met	
	370					375					380					
Gln	Ala	Phe	Asp	Phe	Ser	Tyr	Glu	Met	Glu	Leu	Ser	Thr	Arg	Pro	Ala	
385					390					395					400	
Lys	Ser	Ile	Gly	Asp	Asp	Lys	Val	Trp	Glu	Lys	Ala	Thr	Asn	Ala	Leu	
				405					410					415		
Lys	Glu	Ala	Leu	Lys	Glu	His	Arg	Ile	Asp	Tyr	Lys	Ile	Asp	Glu	Gly	
			420					425					430			
Gly	Gly	Ala	Phe	Tyr	Gly	Pro	Lys	Ile	Asp	Ile	Lys	Ile	Thr	Asp	Ala	
		435					440					445				
Leu	Lys	Arg	Lys	Trp	Gln	Cys	Gly	Thr	Ile	Gln	Val	Asp	Met	Asn	Leu	
	450					455					460					
Pro	Glu	Arg	Phe	Lys	Leu	Ala	Phe	Thr	Asn	Glu	Tyr	Asn	His	Ala	Glu	
465					470					475					480	
Gln	Pro	Val	Met	Ile	His	Arg	Ala	Ile	Leu	Gly	Ser	Phe	Glu	Arg	Phe	
				485					490				495			
Ile	Ala	Ile	Leu	Ser	Glu	His	Phe	Gly	Gly	Asn	Phe	Pro	Phe	Phe	Val	
			500					505					510			
Ala	Pro	Thr	Gln	Ile	Ala	Leu	Ile	Pro	Ile	Asn	Glu	Glu	His	His	Val	
		515					520					525				
Phe	Ala	Leu	Lys	Leu	Lys	Glu	Ala	Leu	Lys	Lys	Arg	Asp	Ile	Phe	Val	
	530					535					540					
Glu	Val	Leu	Asp	Lys	Asn	Asp	Ser	Leu	Asn	Lys	Lys	Val	Arg	Leu	Ala	
545					550					555					560	
Glu	Lys	Gln	Lys	Ile	Pro	Met	Ile	Leu	Val	Leu	Gly	Asn	Glu	Glu	Val	
				565					570					575		
Glu	Thr	Glu	Ile	Leu	Ser	Ile	Arg	Asp	Arg	Glu	Lys	Gln	Asp	Gln	Tyr	
			580					585					590		</	

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<210> 263
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<213> Helicobacter pylori
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<222> (51)...(1145)
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Met Phe
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56

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Lys Val Met Met Gln Met Ala Ile Val Leu Thr Phe Ala Gly Ser Ile	
5 10 15	
ccg atc gtg aaa gtg ggg cgc att gcc ggg caa ttt gcc aag cct cgc	152
Pro Ile Val Lys Val Gly Arg Ile Ala Gly Gln Phe Ala Lys Pro Arg	
20 25 30	
tcc aat gcg act gaa atg ctg gat aat gaa gaa gtg ttg agt tac aga	200
Ser Asn Ala Thr Glu Met Leu Asp Asn Glu Glu Val Leu Ser Tyr Arg	
35 40 45 50	
ggg gat att atc aat ggg att tcc aaa aaa gaa aga gag cca aat cct	248
Gly Asp Ile Ile Asn Gly Ile Ser Lys Lys Glu Arg Glu Pro Asn Pro	
55 60 65	
gaa aga atg ctt aag gcc tac cat caa agc gta gcg act tta aac ctt	296
Glu Arg Met Leu Lys Ala Tyr His Gln Ser Val Ala Thr Leu Asn Leu	
70 75 80	
atc aga gcc ttt gct caa ggc ggg tta gcg gat ttg gag caa gtg cat	344
Ile Arg Ala Phe Ala Gln Gly Gly Leu Ala Asp Leu Glu Gln Val His	
85 90 95	
cgt ttc aat ttg gat ttt gtc aaa aac aac gac ttt ggg caa aaa tac	392
Arg Phe Asn Leu Asp Phe Val Lys Asn Asn Asp Phe Gly Gln Lys Tyr	
100 105 110	
cag caa atc gct gac cgg atc acg caa gct tta ggg ttt atg cga gca	440
Gln Gln Ile Ala Asp Arg Ile Thr Gln Ala Leu Gly Phe Met Arg Ala	
115 120 125 130	
tgc ggg gtg gag ata gag cga acg cct att ctt agg gaa gtg gaa ttt	488
Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val Glu Phe	
135 140 145	
tac acc agc cac gaa gcg tta ctg ctc cat tat gaa gag ccg ttg gtg	536
Tyr Thr Ser His Glu Ala Leu Leu Leu His Tyr Glu Glu Pro Leu Val	
150 155 160	
cgt aag gat agt ctg act aac cag ttt tat gat tgc tcc gcg cac atg	584
Arg Lys Asp Ser Leu Thr Asn Gln Phe Tyr Asp Cys Ser Ala His Met	
165 170 175	
cta tgg att ggc gaa agg aca aga gac cct aag ggt gcg cat gtg gag	632
Leu Trp Ile Gly Glu Arg Thr Arg Asp Pro Lys Gly Ala His Val Glu	
180 185 190	
ttt tta agg ggg gtt tgt aac cct att gcc gtg aaa atc ggg cct aat	680
Phe Leu Arg Gly Val Cys Asn Pro Ile Gly Val Lys Ile Gly Pro Asn	
195 200 205 210	
gcg agc gtg agc gaa gtg tta gaa ttg tgc gat gtt tta aac ccg cgc	728
Ala Ser Val Ser Glu Val Leu Glu Leu Cys Asp Val Leu Asn Pro Arg	
215 220 225	
aac att aag ggg cgt ttg aat ttg atc gtg cgc atg ggt tct aag atg	776
Asn Ile Lys Gly Arg Leu Asn Leu Ile Val Arg Met Gly Ser Lys Met	

230	235	240	
att aaa gag cgt ttg cct aaa ctt tta caa ggg gtg ttg gaa gaa aaa Ile Lys Glu Arg Leu Pro Lys Leu Leu Gln Gly Val Leu Glu Glu Lys 245 250 255			824
cgc cat att tta tgg agc att gat ccc atg cat ggc aac acg gtt aaa Arg His Ile Leu Trp Ser Ile Asp Pro Met His Gly Asn Thr Val Lys 260 265 270			872
acc agc ttg ggg gtt aaa aca agg gct ttt gat agc gtg tta gat gaa Thr Ser Leu Gly Val Lys Thr Arg Ala Phe Asp Ser Val Leu Asp Glu 275 280 285 290			920
gtg aaa agc ttt ttt gaa atc cat agg gct gaa ggg agt ttg gct tca Val Lys Ser Phe Phe Glu Ile His Arg Ala Glu Gly Ser Leu Ala Ser 295 300 305			968
ggg gtt cat ttg gaa atg aca ggt gag aat gtt aca gaa tgt atc ggt Gly Val His Leu Glu Met Thr Gly Glu Asn Val Thr Glu Cys Ile Gly 310 315 320			1016
ggc tcg caa gcg atc acc gaa gag ggt ttg agc tgc cat tac tac acg Gly Ser Gln Ala Ile Thr Glu Glu Gly Leu Ser Cys His Tyr Tyr Thr 325 330 335			1064
caa tgc gat cca aga tta aac gcc acc caa gcc cta gaa ctc gcc ttc Gln Cys Asp Pro Arg Leu Asn Ala Thr Gln Ala Leu Glu Leu Ala Phe 340 345 350			1112
tta atc gct gac atg ctc aaa aaa cag cac gct tagttaaaaa gagattaatc Leu Ile Ala Asp Met Leu Lys Lys Gln His Ala 355 360 365			1165
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<213> Helicobacter pylori			
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Ser Ile Pro Ile Val Lys Val Gly Arg Ile Ala Gly Gln Phe Ala Lys 20 25 30			
Pro Arg Ser Asn Ala Thr Glu Met Leu Asp Asn Glu Glu Val Leu Ser 35 40 45			
Tyr Arg Gly Asp Ile Ile Asn Gly Ile Ser Lys Lys Glu Arg Glu Pro 50 55 60			
Asn Pro Glu Arg Met Leu Lys Ala Tyr His Gln Ser Val Ala Thr Leu 65 70 75 80			
Asn Leu Ile Arg Ala Phe Ala Gln Gly Gly Leu Ala Asp Leu Glu Gln 85 90 95			
Val His Arg Phe Asn Leu Asp Phe Val Lys Asn Asn Asp Phe Gly Gln 100 105 110			
Lys Tyr Gln Gln Ile Ala Asp Arg Ile Thr Gln Ala Leu Gly Phe Met 115 120 125			
Arg Ala Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val			

130	Glu Phe Tyr Thr Ser	135	Glu Ala Leu Leu Leu	140	His Tyr Glu Glu Pro
145	Val Arg Lys Asp Ser	150	Leu Thr Asn Gln Phe	155	Tyr Asp Cys Ser Ala
	165		170		175
His Met Leu Trp Ile Gly	Glu Arg Thr Arg Asp	Pro Lys Gly Ala His			
	180		185		190
Val Glu Phe Leu Arg Gly	Val Cys Asn Pro Ile Gly	Val Lys Ile Gly			
	195		200		205
Pro Asn Ala Ser Val Ser	Glu Val Leu Glu Leu Cys	Asp Val Leu Asn			
	210		215		220
Pro Arg Asn Ile Lys Gly	Arg Leu Asn Leu Ile Val	Arg Met Gly Ser			
	225		230		235
Lys Met Ile Lys Glu Arg	Leu Pro Lys Leu Leu Gln	Gly Val Leu Glu			
	245		250		255
Glu Lys Arg His Ile Leu	Trp Ser Ile Asp Pro Met	His Gly Asn Thr			
	260		265		270
Val Lys Thr Ser Leu Gly	Val Lys Thr Arg Ala Phe	Asp Ser Val Leu			
	275		280		285
Asp Glu Val Lys Ser Phe	Phe Glu Ile His Arg Ala	Glu Gly Ser Leu			
	290		295		300
Ala Ser Gly Val His Leu	Glu Met Thr Gly Glu Asn	Val Thr Glu Cys			
	305		310		315
Ile Gly Gly Ser Gln Ala	Ile Thr Glu Glu Gly Leu	Ser Cys His Tyr			
	325		330		335
Tyr Thr Gln Cys Asp Pro	Arg Leu Asn Ala Thr Gln	Ala Leu Glu Leu			
	340		345		350
Ala Phe Leu Ile Ala Asp	Met Leu Lys Lys Gln His	Ala			
	355		360		365

<210> 265
 <211> 388
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (51)...(335)

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Ala Val Arg Leu Gly Pro Pro Ile Arg Ser Met Phe Val Gly Asn Ala	
	5 10 15
ccg ttt tgg ctt tgg ttt ttt aaa gct tgc atg cct tca ctc aaa ttg	152
Pro Phe Trp Leu Trp Phe Phe Lys Ala Cys Met Pro Ser Leu Lys Leu	
	20 25 30
cgc aca atg gat tct ttt ttc aat aag atg atg caa tta agg gtg atg	200
Arg Thr Met Asp Ser Phe Phe Asn Lys Met Met Gln Leu Arg Val Met	
	35 40 45 50
agc gaa agc aat cgc ggg ctt gca tgc gaa gag acc gcc cca atc atg	248
Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro Ile Met	
	55 60 65

ccc aag ctt gaa atc cca caa acc cca tgc aat aaa gcc gta tca atc 296
Pro Lys Leu Glu Ile Pro Gln Thr Pro Cys Asn Lys Ala Val Ser Ile
70 75 80

tca aac aac tct tca cgc atc gct tca att tct tta tca taaggctgta 345
Ser Asn Asn Ser Ser Arg Ile Ala Ser Ile Ser Leu Ser
85 90 95

aagtaaaatc cttaaagct tcaaaattca aattcaaadc tgt 388

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<211> 95
<212> PRT
<213> Helicobacter pylori

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Asn Ala Pro Phe Trp Leu Trp Phe Phe Lys Ala Cys Met Pro Ser Leu
20 25 30
Lys Leu Arg Thr Met Asp Ser Phe Phe Asn Lys Met Met Gln Leu Arg
35 40 45
Val Met Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro
50 55 60
Ile Met Pro Lys Leu Glu Ile Pro Gln Thr Pro Cys Asn Lys Ala Val
65 70 75 80
Ser Ile Ser Asn Asn Ser Ser Arg Ile Ala Ser Ile Ser Leu Ser
85 90 95

<210> 267
<211> 1756
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(1703)

<400> 267
ttttaagag aactagcact aagagaatat ttttaaaaag ggatttttta gtg cta 56
Val Leu
1

gaa ttt cat caa att tat gat cct ttg ggt aat att tgg ctg agc gct 104
Glu Phe His Gln Ile Tyr Asp Pro Leu Gly Asn Ile Trp Leu Ser Ala
5 10 15

ctt gtg gcc tta ttg ccg att tta ttg ttt ttc tta tct tta atg gtt 152
Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu Met Val
20 25 30

ttt aaa ctc aaa ggt tat aca gcg gcc ttt ttg agc gtg gcc tta tca 200
Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala Leu Ser
35 40 45 50

gcc gtt att gcg gtt tta gtg tat aaa atg cct gtt agc atg gtg ggt 248
Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met Val Gly
55 60 65

tca agc ttc ctt tac ggc ttt ctt tat ggc tta tgg ccg atc gct tgg	296
Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala Trp	
70 75 80	
atc att att gcg gcg att ttt tta tac aaa ctc agc gtt aaa tcc ggc	344
Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys Ser Gly	
85 90 95	
tat ttt gaa att tta aaa gaa agc gtc cag tcc atc act tta gat cac	392
Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu Asp His	
100 105 110	
cgc att tta gtg att ttg att ggc ttt tgt ttt ggc tgc ttt tta gaa	440
Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu Glu	
115 120 125 130	
ggg gcg atc ggc ttt gga ggg cct att gcc att acc gca gcg att tta	488
Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala Ile Leu	
135 140 145	
gtg ggc tta ggg tta agc cct ttg tat tct gcc ggg tta tgt ttg atc	536
Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys Leu Ile	
150 155 160	
gct aat acc gct cct gta gct ttt ggc gcg gtg ggt atc cct ata agt	584
Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro Ile Ser	
165 170 175	
gct atg gcg agc gcg gta ggg gtg cca gcg att tta att tca gcc atg	632
Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser Ala Met	
180 185 190	
acg ggt aaa atc ctc ttt ttt gtg agc ttg tta gtg ccg ttt ttc att	680
Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe Phe Ile	
195 200 205 210	
gtg ttt tta atg gat ggc ttt aaa ggg att aaa gaa act ttt ccg gcc	728
Val Phe Leu Met Asp Gly Phe Lys Gly Ile Lys Glu Thr Phe Pro Ala	
215 220 225	
gtt ttt atc gcg gct ttt tct ttc gct ggt gcg caa ttt tta agc tct	776
Val Phe Ile Ala Ala Phe Ser Phe Ala Gly Ala Gln Phe Leu Ser Ser	
230 235 240	
aat tat tta ggg cca gaa ttg cct ggt att att tca gcc ctt gtt tca	824
Asn Tyr Leu Gly Pro Glu Leu Pro Gly Ile Ile Ser Ala Leu Val Ser	
245 250 255	
ctc gtt gca aca gcg ctc ttt ttg aaa ttt tgg cag cct aaa gcg att	872
Leu Val Ala Thr Ala Leu Phe Leu Lys Phe Trp Gln Pro Lys Ala Ile	
260 265 270	
ttt aga agc gac ggc aaa gcg gct tgc ttc act aag agt aac cat cat	920
Phe Arg Ser Asp Gly Lys Ala Ala Ser Phe Thr Lys Ser Asn His His	
275 280 285 290	
att tgt aag atc tat gtc gct tgg tct cct ttt gtg att tta gtt tta	968
Ile Cys Lys Ile Tyr Val Ala Trp Ser Pro Phe Val Ile Leu Val Leu	

295										300										305										
gtg	att	gtg	cta	tgg	ata	cag	cct	ttt	ttt	aaa	gcc	ttg	ttt	gaa	aaa					1016										
Val	Ile	Val	Leu	Trp	Ile	Gln	Pro	Phe	Phe	Lys	Ala	Leu	Phe	Glu	Lys															
			310					315					320																	
gac	ggc	ttg	tta	gct	ttt	tct	aat	ttt	tat	ttt	gaa	ttc	aat	aac	atc					1064										
Asp	Gly	Leu	Leu	Ala	Phe	Ser	Asn	Phe	Tyr	Phe	Glu	Phe	Asn	Asn	Ile															
		325					330					335																		
agt	aac	cac	atc	ttt	aaa	agc	ccg	cct	ttt	gta	gaa	gcc	aat	caa	agc					1112										
Ser	Asn	His	Ile	Phe	Lys	Ser	Pro	Pro	Phe	Val	Glu	Ala	Asn	Gln	Ser															
	340					345					350																			
gtg	agt	ttt	ccg	gtg	gtg	ttt	aaa	ttt	ctc	tta	atc	aac	acg	gtt	ggc					1160										
Val	Ser	Phe	Pro	Val	Val	Phe	Lys	Phe	Leu	Leu	Ile	Asn	Thr	Val	Gly															
355					360					365					370															
act	tcc	att	ttt	tta	gcc	gct	ctt	gtt	agc	atg	ctc	gtt	tta	agg	gtg					1208										
Thr	Ser	Ile	Phe	Leu	Ala	Ala	Leu	Val	Ser	Met	Leu	Val	Leu	Arg	Val															
				375					380					385																
cga	gtg	agc	gat	gcg	ctg	agc	gtc	ttt	ggc	gag	act	tta	aaa	gaa	atg					1256										
Arg	Val	Ser	Asp	Ala	Leu	Ser	Val	Phe	Gly	Glu	Thr	Leu	Lys	Glu	Met															
			390					395					400																	
cgt	tac	ccc	att	ctc	acc	att	ggc	tta	gtc	tta	agc	ttt	gcc	tat	gtg					1304										
Arg	Tyr	Pro	Ile	Leu	Thr	Ile	Gly	Leu	Val	Leu	Ser	Phe	Ala	Tyr	Val															
		405					410					415																		
tct	aat	tac	agc	ggg	att	tct	tcc	act	cta	gcc	tta	gcg	ctc	acg	cat					1352										
Ser	Asn	Tyr	Ser	Gly	Ile	Ser	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Thr	His															
	420					425					430																			
acg	ggc	ttg	gct	ttc	acc	ttt	ttc	tcg	ccc	ttg	atc	ggg	tgg	gta	ggc					1400										
Thr	Gly	Leu	Ala	Phe	Thr	Phe	Phe	Ser	Pro	Leu	Ile	Gly	Trp	Val	Gly															
435				440					445					450																
gtg	ttt	tta	acc	ggg	agc	gat	acg	agt	tcc	aat	ctt	ttg	ttt	ggc	tct					1448										
Val	Phe	Leu	Thr	Gly	Ser	Asp	Thr	Ser	Ser	Asn	Leu	Leu	Phe	Gly	Ser															
				455				460						465																
tta	cag	caa	ctc	acc	gcc	caa	cga	ttg	cac	ctc	cct	gag	gtt	tta	acc					1496										
Leu	Gln	Gln	Leu	Thr	Ala	Gln	Arg	Leu	His	Leu	Pro	Glu	Val	Leu	Thr															
			470				475						480																	
cta	acg	gct	aat	acc	gtg	ggc	ggc	act	tta	ggc	aag	atg	ata	agc	cct					1544										
Leu	Thr	Ala	Asn	Thr	Val	Gly	Gly	Thr	Leu	Gly	Lys	Met	Ile	Ser	Pro															
		485				490						495																		
caa	agc	atc	gct	atc	gct	tgc	gcg	gcg	gtg	ggg	tta	gcc	ggg	aaa	gag					1592										
Gln	Ser	Ile	Ala	Ile	Ala	Cys	Ala	Ala	Val	Gly	Leu	Ala	Gly	Lys	Glu															
	500					505					510																			
agc	gat	ttg	ttc	aaa	ttc	acg	gtt	aaa	tac	tcc	ctt	att	ttt	gta	gcg					1640										
Ser	Asp	Leu	Phe	Lys	Phe	Thr	Val	Lys	Tyr	Ser	Leu	Ile	Phe	Val	Ala															
515					520					525				530																
atc	atg	gga	gtt	gtg	atc	agc	gcg	att	gcg	tat	ttg	atc	cct	gaa	gtg					1688										

[illegible]

1743

1756

<400> 268

Gln Ser Val Ser Phe Pro Val Val Phe Lys Phe Leu Leu Ile Asn Thr
 355 360 365
 Val Gly Thr Ser Ile Phe Leu Ala Ala Leu Val Ser Met Leu Val Leu
 370 375 380
 Arg Val Arg Val Ser Asp Ala Leu Ser Val Phe Gly Glu Thr Leu Lys
 385 390 395 400
 Glu Met Arg Tyr Pro Ile Leu Thr Ile Gly Leu Val Leu Ser Phe Ala
 405 410 415
 Tyr Val Ser Asn Tyr Ser Gly Ile Ser Ser Thr Leu Ala Leu Ala Leu
 420 425 430
 Thr His Thr Gly Leu Ala Phe Thr Phe Phe Ser Pro Leu Ile Gly Trp
 435 440 445
 Val Gly Val Phe Leu Thr Gly Ser Asp Thr Ser Ser Asn Leu Leu Phe
 450 455 460
 Gly Ser Leu Gln Gln Leu Thr Ala Gln Arg Leu His Leu Pro Glu Val
 465 470 475 480
 Leu Thr Leu Thr Ala Asn Thr Val Gly Gly Thr Leu Gly Lys Met Ile
 485 490 495
 Ser Pro Gln Ser Ile Ala Ile Ala Cys Ala Ala Val Gly Leu Ala Gly
 500 505 510
 Lys Glu Ser Asp Leu Phe Lys Phe Thr Val Lys Tyr Ser Leu Ile Phe
 515 520 525
 Val Ala Ile Met Gly Val Val Ile Ser Ala Ile Ala Tyr Leu Ile Pro
 530 535 540
 Glu Val Val Pro Ala Ile Lys
 545 550

<210> 269
 <211> 961
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (51)...(908)

<400> 269
 tgaaccacgc cataaaaaag ttcattgataa tggcataaag gaaagttgaa atg gat 56
 Met Asp
 1
 ttt tta aac gac cat ata aat gtt ttt ggc ttg att gca gcg ctt gtg 104
 Phe Leu Asn Asp His Ile Asn Val Phe Gly Leu Ile Ala Ala Leu Val
 5 10 15
 att tta gtt tta acc atc tat gaa tcc agt tcg ctc att aaa gaa atg 152
 Ile Leu Val Leu Thr Ile Tyr Glu Ser Ser Ser Leu Ile Lys Glu Met
 20 25 30
 cgc gac agc aaa tct caa ggt gag ctt gta gaa aat ggg cat ttg att 200
 Arg Asp Ser Lys Ser Gln Gly Glu Leu Val Glu Asn Gly His Leu Ile
 35 40 45 50
 gat ggg ata ggg gag ttt gcc aat aat gtg cca gta ggc tgg atc gca 248
 Asp Gly Ile Gly Glu Phe Ala Asn Asn Val Pro Val Gly Trp Ile Ala
 55 60 65
 agc ttt atg tgc acg att gtg tgg gct ttt tgg tat ttc ttc ttt ggg 296
 Ser Phe Met Cys Thr Ile Val Trp Ala Phe Trp Tyr Phe Phe Phe Gly

<213> Helicobacter pylori

<400> 270

Met	Asp	Phe	Leu	Asn	Asp	His	Ile	Asn	Val	Phe	Gly	Leu	Ile	Ala	Ala
1				5					10					15	
Leu	Val	Ile	Leu	Val	Leu	Thr	Ile	Tyr	Glu	Ser	Ser	Ser	Leu	Ile	Lys
			20					25					30		
Glu	Met	Arg	Asp	Ser	Lys	Ser	Gln	Gly	Glu	Leu	Val	Glu	Asn	Gly	His
		35				40						45			
Leu	Ile	Asp	Gly	Ile	Gly	Glu	Phe	Ala	Asn	Asn	Val	Pro	Val	Gly	Trp
50						55					60				
Ile	Ala	Ser	Phe	Met	Cys	Thr	Ile	Val	Trp	Ala	Phe	Trp	Tyr	Phe	Phe
65					70					75					80
Phe	Gly	Tyr	Pro	Leu	Asn	Ser	Phe	Ser	Gln	Ile	Gly	Gln	Tyr	Asn	Glu
				85					90					95	
Glu	Val	Lys	Ala	His	Asn	Gln	Lys	Phe	Glu	Ala	Lys	Trp	Lys	His	Leu
			100					105					110		
Gly	Gln	Lys	Glu	Leu	Val	Asp	Met	Gly	Gln	Gly	Ile	Phe	Leu	Val	His
		115					120					125			
Cys	Ser	Gln	Cys	His	Gly	Ile	Thr	Ala	Glu	Gly	Leu	His	Gly	Ser	Ala
130						135					140				
Gln	Asn	Leu	Val	Arg	Trp	Gly	Lys	Glu	Glu	Gly	Ile	Met	Asp	Thr	Ile
145					150					155					160
Lys	His	Gly	Ser	Lys	Gly	Met	Asp	Tyr	Leu	Ala	Gly	Glu	Met	Pro	Ala
				165				170						175	
Met	Glu	Leu	Asp	Glu	Lys	Asp	Ala	Lys	Ala	Ile	Ala	Ser	Tyr	Val	Met
			180					185					190		
Ala	Glu	Leu	Ser	Ser	Val	Lys	Lys	Thr	Lys	Asn	Pro	Gln	Leu	Ile	Asp
		195					200					205			
Lys	Gly	Lys	Glu	Leu	Phe	Glu	Ser	Met	Gly	Cys	Thr	Gly	Cys	His	Gly
	210					215						220			
Asn	Asp	Gly	Lys	Gly	Leu	Gln	Glu	Asn	Gln	Val	Phe	Ala	Ala	Asp	Leu
225					230					235					240
Thr	Ala	Tyr	Gly	Thr	Glu	Asn	Phe	Leu	Arg	Asn	Ile	Leu	Thr	His	Gly
				245					250					255	
Lys	Lys	Gly	Asn	Ile	Gly	His	Met	Pro	Ser	Phe	Lys	Tyr	Lys	Asn	Phe
			260					265					270		
Ser	Asp	Leu	Gln	Val	Lys	Ala	Leu	Leu	Asn	Leu	Ser	Asn	Arg		
		275					280					285			

<210> 271

<211> 307

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(254)

<400> 271

tactgaattt atccaatcgc taaaaccctt agaagattaa aggaaaagag atg aaa	56
Met Lys	
1	
ttt tta aac gga tta gca ggg aat tta ctg att gtg gtt att tta ttg	104
Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile Leu Leu	
5 10 15	
tgt gtg gcc gtt ttt ttt acg ctc aaa gcg atc cat atc caa aaa gag	152

Cys Val Ala Val Phe Phe Thr Leu Lys Ala Ile His Ile Gln Lys Glu
 20 25 30

caa gcc acc aat tat tac cgc tat aag gat att aac gct tta gag aca 200
 Gln Ala Thr Asn Tyr Tyr Arg Tyr Lys Asp Ile Asn Ala Leu Glu Thr
 35 40 45 50

aaa aac acc caa aac cgg gct aac tat gaa tta gtc aat caa ggg agt 248
 Lys Asn Thr Gln Asn Arg Ala Asn Tyr Glu Leu Val Asn Gln Gly Ser
 55 60 65

aaa aaa tgaaattcac gacttttagaa aaaatttttag ctttgatggg agtagcgacc 304
 Lys Lys

att 307

<210> 272
 <211> 68
 <212> PRT
 <213> Helicobacter pylori

<400> 272
 Met Lys Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile
 1 5 10 15
 Leu Leu Cys Val Ala Val Phe Phe Thr Leu Lys Ala Ile His Ile Gln
 20 25 30
 Lys Glu Gln Ala Thr Asn Tyr Tyr Arg Tyr Lys Asp Ile Asn Ala Leu
 35 40 45
 Glu Thr Lys Asn Thr Gln Asn Arg Ala Asn Tyr Glu Leu Val Asn Gln
 50 55 60
 Gly Ser Lys Lys
 65

<210> 273
 <211> 843
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(770)

<400> 273
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 Met Gly
 1

cga gcg ttt gaa tac aga aga gcg gct aaa gaa aaa cga tgg gat aag 104
 Arg Ala Phe Glu Tyr Arg Arg Ala Ala Lys Glu Lys Arg Trp Asp Lys
 5 10 15

atg agt aag gtt ttc cca aag ctc gct aaa gcg atc act cta gcg gca 152
 Met Ser Lys Val Phe Pro Lys Leu Ala Lys Ala Ile Thr Leu Ala Ala
 20 25 30

aaa gat ggc ggg agc gaa ccg gac acg aac gcc aaa cta cga aca gcg 200
 Lys Asp Gly Gly Ser Glu Pro Asp Thr Asn Ala Lys Leu Arg Thr Ala
 35 40 45 50

att tta aac gct aaa gcg caa aac atg cct aaa gac aat att gac gca Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile Asp Ala 55 60 65	248
gcg att aaa aga gcg agc agt aaa gaa ggg aat ttg agt gaa atc act Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu Ile Thr 70 75 80	296
tat gaa ggt aag gcg aat ttt ggc gtg cta atc atc atg gaa tgc atg Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu Cys Met 85 90 95	344
act gat aac ccc acc aga acc att gcc aac ctt aaa agc tat ttc aat Thr Asp Asn Pro Thr Arg Thr Ile Ala Asn Leu Lys Ser Tyr Phe Asn 100 105 110	392
aaa acg caa ggg gca agc atc gtg cct aat ggc tct tta gag ttt atg Lys Thr Gln Gly Ala Ser Ile Val Pro Asn Gly Ser Leu Glu Phe Met 115 120 125 130	440
ttt aac cga aaa agc gtg ttt gaa tgc ttg aaa aat gaa gtg gaa aat Phe Asn Arg Lys Ser Val Phe Glu Cys Leu Lys Asn Glu Val Glu Asn 135 140 145	488
tta aaa ctc agt cta gaa gat tta gaa ttc gct ctc att gat tat ggt Leu Lys Leu Ser Leu Glu Asp Leu Glu Phe Ala Leu Ile Asp Tyr Gly 150 155 160	536
ttg gaa gaa tta gaa gaa gtg gaa gac aag atc att att agg ggg gat Leu Glu Glu Leu Glu Glu Val Glu Asp Lys Ile Ile Ile Arg Gly Asp 165 170 175	584
tat aac agc ttc aag ctt tta aat gag ggg ttt gaa agc ttg aaa tta Tyr Asn Ser Phe Lys Leu Leu Asn Glu Gly Phe Glu Ser Leu Lys Leu 180 185 190	632
ccc att tta aaa gcg agt ttg caa cgc atc gcc aca acg ccc att gaa Pro Ile Leu Lys Ala Ser Leu Gln Arg Ile Ala Thr Thr Pro Ile Glu 195 200 205 210	680
ttg aat gac gaa caa atg gag ctt acc gaa aaa tta ctg gac agg att Leu Asn Asp Glu Gln Met Glu Leu Thr Glu Lys Leu Leu Asp Arg Ile 215 220 225	728
gaa gac gat gat gat gtg gtc gcg ctt tat acc aat att gag Glu Asp Asp Asp Val Val Ala Leu Tyr Thr Asn Ile Glu 230 235 240	770
tgaaatgcaa aaagactcaa agtatttttt taaaccaccc aagcattcat cccaataggg aatgcgttgg aga	830 843

<210> 274

<211> 240

<212> PRT

<213> Helicobacter pylori

<400> 274

Met Gly Arg Ala Phe Glu Tyr Arg Arg Ala Ala Lys Glu Lys Arg Trp

50	55	60	65	
ggc tct tgc gcg atg atg gtt aat ggg aga ccg agg cta gct tgt aaa				296
Gly Ser Cys Ala Met Met Val Asn Gly Arg Pro Arg Leu Ala Cys Lys	70	75	80	
acc cta act tct agc ttt gaa agc ggg gtg atc acg ctc atg ccc atg				344
Thr Leu Thr Ser Ser Phe Glu Ser Gly Val Ile Thr Leu Met Pro Met	85	90	95	
ccc agt ttt acg ctc att aaa gat ttg agc gtg aat acg ggc gat tgg				392
Pro Ser Phe Thr Leu Ile Lys Asp Leu Ser Val Asn Thr Gly Asp Trp	100	105	110	
ttt ttg gat atg act aaa agg gtg gag agt tgg gcg cat tct aaa gaa				440
Phe Leu Asp Met Thr Lys Arg Val Glu Ser Trp Ala His Ser Lys Glu	115	120	125	
gaa gtg gat att act aga ccg gaa aaa agg gtt gag cct gac gaa gcc				488
Glu Val Asp Ile Thr Arg Pro Glu Lys Arg Val Glu Pro Asp Glu Ala	130	135	140	145
caa gaa gtc ttt gaa cta gac agg tgt att gaa tgc ggg tgt tgt atc				536
Gln Glu Val Phe Glu Leu Asp Arg Cys Ile Glu Cys Gly Cys Cys Ile	150	155	160	
gct tct tgc ggg act aaa ctc atg cgc cct aat ttc att gga gct gct				584
Ala Ser Cys Gly Thr Lys Leu Met Arg Pro Asn Phe Ile Gly Ala Ala	165	170	175	
ggc atg aac aga gcc atg cgt ttt atg att gac agc cac gat gaa aga				632
Gly Met Asn Arg Ala Met Arg Phe Met Ile Asp Ser His Asp Glu Arg	180	185	190	
aac gat gat gat ttt tat gag tta gtc ggc gat gat gat ggt gtt ttt				680
Asn Asp Asp Asp Phe Tyr Glu Leu Val Gly Asp Asp Asp Gly Val Phe	195	200	205	
ggg tgc atg agc ctt atc gct tgc cat gac act tgc cc taaagaatta				728
Gly Cys Met Ser Leu Ile Ala Cys His Asp Thr Cys	210	215	220	
cccttgcaaa gcagtatcgc cacttttgcgt aacaggatgt tgaaagtggg taaaagccgc				788
taattttcttt ttagtggggtc gttttttgaaa atcttttttag tctttttaag cg				840

<210> 278

<211> 222

<212> PRT

<213> Helicobacter pylori

<400> 278

Met Ser Asp Asn Glu Arg Thr Ile Val Val Arg Val Leu Lys Phe Asp	1	5	10	15
Pro Gln Ser Ala Val Ser Lys Pro His Phe Lys Glu Tyr Gln Leu Lys	20	25	30	
Glu Thr Pro Ser Met Thr Leu Phe Ile Ala Leu Asn Leu Ile Arg Glu	35	40	45	
His Gln Asp Pro Asp Leu Ser Phe Asp Phe Val Cys Arg Ala Gly Ile	50	55	60	

Cys Gly Ser Cys Ala Met Met Val Asn Gly Arg Pro Arg Leu Ala Cys
65 70 75 80
Lys Thr Leu Thr Ser Ser Phe Glu Ser Gly Val Ile Thr Leu Met Pro
85 90 95
Met Pro Ser Phe Thr Leu Ile Lys Asp Leu Ser Val Asn Thr Gly Asp
100 105 110
Trp Phe Leu Asp Met Thr Lys Arg Val Glu Ser Trp Ala His Ser Lys
115 120 125
Glu Glu Val Asp Ile Thr Arg Pro Glu Lys Arg Val Glu Pro Asp Glu
130 135 140
Ala Gln Glu Val Phe Glu Leu Asp Arg Cys Ile Glu Cys Gly Cys Cys
145 150 155 160
Ile Ala Ser Cys Gly Thr Lys Leu Met Arg Pro Asn Phe Ile Gly Ala
165 170 175
Ala Gly Met Asn Arg Ala Met Arg Phe Met Ile Asp Ser His Asp Glu
180 185 190
Arg Asn Asp Asp Asp Phe Tyr Glu Leu Val Gly Asp Asp Asp Gly Val
195 200 205
Phe Gly Cys Met Ser Leu Ile Ala Cys His Asp Thr Cys Pro
210 215 220

<210> 279
<211> 351
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (53)...(262)

<400> 279
gaaagccaaa gtagccctt gattgaaaca agattgagcg atcccataag cg atg gat 58
Met Asp
1

tta ttg ttc gcc acc cct aca ata agc cct ttt tta cct ttt aaa aat 106
Leu Leu Phe Ala Thr Pro Thr Ile Ser Pro Phe Leu Pro Phe Lys Asn
5 10 15

ccc atg att ttc ctt tat aaa aat gaa atg att gtt tta aaa ttt tct 154
Pro Met Ile Phe Leu Tyr Lys Asn Glu Met Ile Val Leu Lys Phe Ser
20 25 30

aat tcc caa gac gcg ctc ccg atc aac aag cca tcc acg cta tca atc 202
Asn Ser Gln Asp Ala Leu Pro Ile Asn Lys Pro Ser Thr Leu Ser Ile
35 40 45 50

cct aaa att tct tta gcg ttt tgt gtg ttc acg ctc ccc cca tac aac 250
Pro Lys Ile Ser Leu Ala Phe Cys Val Phe Thr Leu Pro Pro Tyr Asn
55 60 65

aag ggc gtt ttt tgatttaaga tttgctttaa aaaaccatgc gtgagataaa 302
Lys Gly Val Phe
70

tatcttctaa agaagcgctt tttttggtgc caatcgccca aataggctc 351

<210> 280
<211> 70

<212> PRT
 <213> Helicobacter pylori

<400> 280

Met	Asp	Leu	Leu	Phe	Ala	Thr	Pro	Thr	Ile	Ser	Pro	Phe	Leu	Pro	Phe
1				5					10				15		
Lys	Asn	Pro	Met	Ile	Phe	Leu	Tyr	Lys	Asn	Glu	Met	Ile	Val	Leu	Lys
			20					25					30		
Phe	Ser	Asn	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Asn	Lys	Pro	Ser	Thr	Leu
		35				40					45				
Ser	Ile	Pro	Lys	Ile	Ser	Leu	Ala	Phe	Cys	Val	Phe	Thr	Leu	Pro	Pro
	50					55					60				
Tyr	Asn	Lys	Gly	Val	Phe										
65					70										

<210> 281
 <211> 1271
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (368)...(1210)

<400> 281

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gtatccctgc	tggcgtgagc	ttattttcca	tgctagcaaa	cgccaaacga	gagagagaga	120
gagagagaga	gtaaaactct	tttatcaaat	ccattgtttg	gtggagagtt	taaccccaga	180
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ttctaaa	atg atc atg tgc cgt ttc ttt ttt gcc	tcc ctt ttc ccc caa	409			
	Met Ile Met Cys Arg Phe Phe Phe Ala	Ser Leu Phe Pro Gln				
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tac gat aag atg atc atg ttt gat gtg gac act ttg ttt gtg aat gat	457					
Tyr Asp Lys Met Ile Met Phe Asp Val Asp Thr Leu Phe Val Asn Asp						
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att agc gag agc ttt ttt atc ccc ctt gaa acg cat tat ttt ggg gct	505					
Ile Ser Glu Ser Phe Phe Ile Pro Leu Glu Thr His Tyr Phe Gly Ala						
	35	40	45			
gtg agg gaa aaa gat ttg atc gct ata aat agg aat tcg gct aag gat	553					
Val Arg Glu Lys Asp Leu Ile Ala Ile Asn Arg Asn Ser Ala Lys Asp						
	50	55	60			
tta tac gaa ttg cgc caa atg cat gca aaa tct atc ggc atc gcc aac	601					
Leu Tyr Glu Leu Arg Gln Met His Ala Lys Ser Ile Gly Ile Ala Asn						
	65	70	75			
gct ttc cct aat tta gaa gaa gct caa atc ctt ttt gac aac tac ttt	649					
Ala Phe Pro Asn Leu Glu Glu Ala Gln Ile Leu Phe Asp Asn Tyr Phe						
	80	85	90			
aac gcc ggg ttt tta gcc tta aat tta aaa tca tgg cgt aaa gaa aat	697					
Asn Ala Gly Phe Leu Ala Leu Asn Leu Lys Ser Trp Arg Lys Glu Asn						
	95	100	105	110		

ctt gaa aac caa ttg att acc ttt ttc att ttg aaa aat gaa aaa ctt 745
 Leu Glu Asn Gln Leu Ile Thr Phe Phe Ile Leu Lys Asn Glu Lys Leu
 115 120 125

 tta ttt aac gat caa gat gct ttg tgt ttt gtg tgc cgt ggg agg att 793
 Leu Phe Asn Asp Gln Asp Ala Leu Cys Phe Val Cys Arg Gly Arg Ile
 130 135 140

 tta gaa ttg cct tat cca tac aat gcc cac cct agt ttc ctt gat acg 841
 Leu Glu Leu Pro Tyr Pro Tyr Asn Ala His Pro Ser Phe Leu Asp Thr
 145 150 155

 ctc tca ttc cct agc atc aaa gaa gcg cgc atg ctg cat ttt tgg ggc 889
 Leu Ser Phe Pro Ser Ile Lys Glu Ala Arg Met Leu His Phe Trp Gly
 160 165 170

 gat aaa ccc tgg aaa ctc tta agc gtc att ggc gcg aaa aaa tgg cat 937
 Asp Lys Pro Trp Lys Leu Leu Ser Val Ile Gly Ala Lys Lys Trp His
 175 180 185 190

 gaa gcg ttg atc caa acg cct ttt aaa gac gcc tat ttc aac gct tct 985
 Glu Ala Leu Ile Gln Thr Pro Phe Lys Asp Ala Tyr Phe Asn Ala Ser
 195 200 205

 ttt tta gat cac ctc ttt gaa tcc ctt caa aac aag gat aat gag atc 1033
 Phe Leu Asp His Leu Phe Glu Ser Leu Gln Asn Lys Asp Asn Glu Ile
 210 215 220

 aaa aga aga gat gaa agg atc att gaa gca ctt caa gca agg gat aaa 1081
 Lys Arg Arg Asp Glu Arg Ile Ile Glu Ala Leu Gln Ala Arg Asp Lys
 225 230 235

 atc ctg tct ttt tca gac aag cga cat tct ttt gaa tct ctt ctg ccc 1129
 Ile Leu Ser Phe Ser Asp Lys Arg His Ser Phe Glu Ser Leu Leu Pro
 240 245 250

 aag ctt tct tct aaa ctc ctt ata gaa ttt ttg ctt ttt aaa gcc aaa 1177
 Lys Leu Ser Ser Lys Leu Leu Ile Glu Phe Leu Leu Phe Lys Ala Lys
 255 260 265 270

 caa aaa gtg aag cga ctg att aaa agg gtt ttt taaaaccctt tttaaactaa 1230
 Gln Lys Val Lys Arg Leu Ile Lys Arg Val Phe
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 <212> PRT
 <213> Helicobacter pylori

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 Lys Met Ile Met Phe Asp Val Asp Thr Leu Phe Val Asn Asp Ile Ser
 20 25 30
 Glu Ser Phe Phe Ile Pro Leu Glu Thr His Tyr Phe Gly Ala Val Arg
 35 40 45
 Glu Lys Asp Leu Ile Ala Ile Asn Arg Asn Ser Ala Lys Asp Leu Tyr

tgc Cys	ttg Leu	aaa Lys	aaa Lys	ggc Gly	aaa Lys	aac Asn	cat His	att Ile	gta Val	acc Thr	acg Thr	gtt Val	gca Ala	gag Glu	cat His	296
707580																
ccg Pro	gcg Ala	gtg Val	cga Arg	tcc Ser	act Thr	tgc Cys	aat Asn	ttt Phe	tta Leu	gaa Glu	agc Ser	ttg Leu	ggg Gly	gtg Val	gag Glu	344
859095																
gtt Val	act Thr	tac Tyr	ttg Leu	ccc Pro	att Ile	aat Asn	gag Glu	cat His	ggg Gly	agc Ser	atc Ile	acc Thr	gca Ala	gag Glu	caa Gln	392
100105110																
gtc Val	aaa Lys	gaa Glu	gcg Ala	atc Ile	aca Thr	gaa Glu	aaa Lys	acc Thr	gct Ala	cta Leu	gtg Val	agc Ser	gtg Val	atg Met	tgg Trp	440
115120125130																
gcg Ala	aat Asn	aat Asn	gaa Glu	acc Thr	ggt Gly	ctc Leu	att Ile	ttc Phe	cct Pro	att Ile	gaa Glu	gaa Glu	att Ile	ggg Gly	gct Ala	488
135140145																
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att Ile	ggt Gly	aaa Lys	atc Ile	cct Pro	gta Val	gat Asp	gtg Val	tta Leu	aaa Lys	gcg Ala	aat Asn	gca Ala	gat Asp	ttc Phe	ctt Leu	584
165170175																
tct Ser	ttt Phe	agc Ser	gcg Ala	cac His	aag Lys	ttt Phe	cat His	ggg Gly	cct Pro	aaa Lys	ggc Gly	att Ile	ggg Gly	ggg Gly	ttg Leu	632
180185190																
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cat His	atg Met	aat Asn	ggc Gly	agg Arg	cgc Arg	agc Ser	ggg Gly	act Thr	ttg Leu	aat Asn	gtg Val	cct Pro	tat Tyr	att Ile	gtg Val	728
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230235240																
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aaa Lys	atc Ile	cct Pro	gat Asp	gtg Val	atg Met	gtg Val	gtg Val	ggc Gly	gat Asp	aga Arg	atc Ile	cat His	cgt Arg	gtg Val	cct Pro	872
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aac Asn	acg Thr	act Thr	tta Leu	gtc Val	agc Ser	gtg Val	aga Arg	ggg Gly	att Ile	gaa Glu	gga Gly	gag Glu	gcc Ala	atg Met	ctg Leu	920
275280285290																
tgg Trp	gat Asp	tta Leu	aac Asn	cgc Arg	tct Ser	aat Asn	atc Ile	gcc Ala	gct Ala	tcc Ser	aca Thr	ggg Gly	agc Ser	gcg Ala	tgc Cys	968

gcg cta ggc att ttg ctt tta atg gag caa ttc aaa ttc ctt caa aac Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu Gln Asn 135 140 145	488
caa aat ttg ggg gtg ttt gtc ttg ctc gct att ggg ata ctc atc att Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu Ile Ile 150 155 160	536
tat ctt ttt cct cta atc act aaa aaa atc ccc tct aat ctg att tgt Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu Ile Cys 165 170 175	584
atc ctt ata gtg agc gcg atc gct tta att ttt gat atg cat gcg ccg Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His Ala Pro 180 185 190	632
aat ttg ggg agc att gag caa ggg gtt tca ggc ttt cat ttc atc att Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe Ile Ile 195 200 205 210	680
atc ccc aaa aat ttg gat ttt aaa ata atg ata gag ttg ttg cct tac Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu Pro Tyr 215 220 225	728
gct ctt tct tta gca cta gtg gga acg ata gaa agc tta ttg acg gct Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu Thr Ala 230 235 240	776
aaa act tta gat gtg att tta aaa gac ggc gtg agc gat aaa aat aaa Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys Asn Lys 245 250 255	824
gaa act aaa gcg caa ggc ttg ggg aat atc atc tca ggg ctt ttg ggg Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu Leu Gly 260 265 270	872
gga atg aca ggg tgc gct tta gtg ggg cag tct atc att aac gca aaa Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn Ala Lys 275 280 285 290	920
tcc ggg gct aaa aca agg ctt tct act ttt ttt gcc ggc ttt tct tta Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe Ser Leu 295 300 305	968
atg gtg ctc ata tta gtg ttt aat gaa tat gtg gtt aag atc ccc att Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile Pro Ile 310 315 320	1016
gtg gcg gtt gtg gcg gta atg gtg atg att tct ttc acc act ttt aat Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr Phe Asn 325 330 335	1064
ttc caa tcc att att aac att aaa aaa atc aag ctc tat gac acg ctc Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp Thr Leu 340 345 350	1112
aac atg ctc tta gtc gtg gcg gtg gtt tta tac acg cat aat tta gcg Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn Leu Ala	1160

355	360	365	370	
ata ggg gtt gtg gtg ggg gtt tta gtc aat gcg tta tgg atc aaa tct				1208
Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile Lys Ser				
375	380	385		
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Lys Gly Ile Ala				
390				
ctccagatgt agg				1273
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Ile Pro Glu Thr Ala Gly Phe Ala Ile Met Val Gly Leu Asp Val Gly				
35 40 45				
Val Ala Phe Tyr Thr Thr Phe Tyr Met Ala Phe Val Leu Ser Leu Phe				
50 55 60				
Gly Ala Arg Lys Ala Met Ile Ser Ala Ala Ala Gly Ser Val Ala Leu				
65 70 75 80				
Ile Leu Val Gly Val Val Lys Asn Tyr Gly Leu Glu Tyr Ala Gly Val				
85 90 95				
Ala Thr Leu Met Ala Gly Val Leu Gln Ile Leu Leu Gly Tyr Leu Lys				
100 105 110				
Ile Gly Asn Leu Leu Arg Phe Ile Pro Gln Ser Val Met Tyr Gly Phe				
115 120 125				
Val Asn Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu				
130 135 140				
Gln Asn Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu				
145 150 155 160				
Ile Ile Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu				
165 170 175				
Ile Cys Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His				
180 185 190				
Ala Pro Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe				
195 200 205				
Ile Ile Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu				
210 215 220				
Pro Tyr Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu				
225 230 235 240				
Thr Ala Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys				
245 250 255				
Asn Lys Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu				
260 265 270				
Leu Gly Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn				
275 280 285				
Ala Lys Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe				
290 295 300				
Ser Leu Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile				
305 310 315 320				
Pro Ile Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr				

325 330 335
 Phe Asn Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp
 340 345 350
 Thr Leu Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn
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 Leu Ala Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile
 370 375 380
 Lys Ser Lys Gly Ile Ala
 385 390

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 gaaaaaagaa tgcttgatag aaagcgaaat tcaaatcggt aagactaagg gcgataaaat 180
 cttagacacc cctttaaata agatcggcgg taaggggcta ttcactaagg aattagaaga 240
 attgctttta aagggcgcaa ttgatttggc ggtgcattct ttaaaagacg tgccgggtcgt 300
 gtttgaaaag gggtagact tggcatgcat caccaaaagg gctgatgtga gggacacttt 360
 ttttagcgtg aaattccctg atttg atg agt ttg cct aaa ggg gca aag gtt 412
 Met Ser Leu Pro Lys Gly Ala Lys Val
 1 5
 ggc acg act tct tta agg cgc tct atg cag atc aaa tta aag cgc cag 460
 Gly Thr Thr Ser Leu Arg Arg Ser Met Gln Ile Lys Leu Lys Arg Gln
 10 15 20 25
 gat ttg gac aca gaa agc ttg aga ggg aat gtc caa acc cgt ttg aaa 508
 Asp Leu Asp Thr Glu Ser Leu Arg Gly Asn Val Gln Thr Arg Leu Lys
 30 35 40
 aag ctt gaa tgc gga gaa ttt gac gct atc att tta gct gaa gcc ggg 556
 Lys Leu Glu Cys Gly Glu Phe Asp Ala Ile Ile Leu Ala Glu Ala Gly
 45 50 55
 ttg tgc cgc cta gaa att caa gga gcg aaa tac cgc aag gct ttt agc 604
 Leu Cys Arg Leu Glu Ile Gln Gly Ala Lys Tyr Arg Lys Ala Phe Ser
 60 65 70
 gta gaa gaa atg att cct agc atg ggt cag ggg gct tta ggg gta gaa 652
 Val Glu Glu Met Ile Pro Ser Met Gly Gln Gly Ala Leu Gly Val Glu
 75 80 85
 atg ctc aaa aac cac aag cat ttt gcc acg ctt caa aaa ctc aac gac 700
 Met Leu Lys Asn His Lys His Phe Ala Thr Leu Gln Lys Leu Asn Asp
 90 95 100 105
 gag aaa agc gcg ttt tgc tgc cgt tta gaa agg gag ttt atc aag ggg 748
 Glu Lys Ser Ala Phe Cys Cys Arg Leu Glu Arg Glu Phe Ile Lys Gly
 110 115 120
 ctt aat gga ggg tgt cag atc cct ata ggc gtg cat gcg agt tta atg 796

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gct gta acc atc ttt cat gat aaa ttc cct cgc tct cac cag ccc aaa 104
Ala Val Thr Ile Phe His Asp Lys Phe Pro Arg Ser His Gln Pro Lys
5 10 15

tct tgg gcg gat ttc atc acg gaa ttt cgt gtg gat ttg ata gag atg 152
Ser Trp Ala Asp Phe Ile Thr Glu Phe Arg Val Asp Leu Ile Glu Met
20 25 30

gac ggg caa ttg ctt gta act ttt aat gaa att agc ggc aat ttc ggt 200
Asp Gly Gln Leu Leu Val Thr Phe Asn Glu Ile Ser Gly Asn Phe Gly
35 40 45 50

gat att ttc ttc taaagtgggg cttaaaacaa aatcattgtc ttttcgggtct 252
Asp Ile Phe Phe

ttaaaaaacca ata 265

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<213> Helicobacter pylori
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[illegible]

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<212> DNA
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           Met Ala Asp Val Val Gly Ile Gln Trp Gly Asp Glu
                1             5             10

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ggg aag gga aaa att gtt gat agg atc gct aaa gat tat gac ttt gtg 159
Gly Lys Gly Lys Ile Val Asp Arg Ile Ala Lys Asp Tyr Asp Phe Val

15	20	25	
gtg cgc tat cag ggc ggg cat aat gct ggg cat acc att gtg cat aag			207
Val Arg Tyr Gln Gly Gly His Asn Ala Gly His Thr Ile Val His Lys			
30	35	40	45
ggg gtt aag cat tct ttg cat tta atg cct tca ggg gtt tta tac ccc			255
Gly Val Lys His Ser Leu His Leu Met Pro Ser Gly Val Leu Tyr Pro			
	50	55	60
aaa tgc aag aac atc att tct agc gcg gtg gtc gtg agc gtt aag gat			303
Lys Cys Lys Asn Ile Ile Ser Ser Ala Val Val Val Ser Val Lys Asp			
	65	70	75
ttg tgc gaa gaa atc agc gcg ttt gag gat tta gaa aat cgt ttg ttt			351
Leu Cys Glu Glu Ile Ser Ala Phe Glu Asp Leu Glu Asn Arg Leu Phe			
	80	85	90
gtc agc gac aga gcc cat gtg atc ttg ccc tat cat gcc aaa aaa gac			399
Val Ser Asp Arg Ala His Val Ile Leu Pro Tyr His Ala Lys Lys Asp			
	95	100	105
gct ttt aaa gaa aaa tct caa aac atc ggc acg act aaa aaa ggc ata			447
Ala Phe Lys Glu Lys Ser Gln Asn Ile Gly Thr Thr Lys Lys Gly Ile			
110	115	120	125
ggc cct tgc tat gag gat aaa atg gcc agg agc ggg ata aga atg ggg			495
Gly Pro Cys Tyr Glu Asp Lys Met Ala Arg Ser Gly Ile Arg Met Gly			
	130	135	140
gat tta tta gac gat aaa atc tta gaa gaa aag cta aac gct cat ttc			543
Asp Leu Leu Asp Asp Lys Ile Leu Glu Glu Lys Leu Asn Ala His Phe			
	145	150	155
aaa gcc att gag cct ttt aaa aaa gcg tat gat ttg ggc gag aat tac			591
Lys Ala Ile Glu Pro Phe Lys Lys Ala Tyr Asp Leu Gly Glu Asn Tyr			
	160	165	170
gaa aaa gat ttg atg ggg tat ttt aaa act tac gct cca aaa att tgc			639
Glu Lys Asp Leu Met Gly Tyr Phe Lys Thr Tyr Ala Pro Lys Ile Cys			
	175	180	185
ccc ttt atc aaa gac acg aca agc atg ctg ata gaa gcg aat caa aag			687
Pro Phe Ile Lys Asp Thr Thr Ser Met Leu Ile Glu Ala Asn Gln Lys			
190	195	200	205
ggt gaa aaa atc cta tta gaa ggg gca caa ggc acg ctt tta gac att			735
Gly Glu Lys Ile Leu Leu Glu Gly Ala Gln Gly Thr Leu Leu Asp Ile			
	210	215	220
gat tta ggg act tac cct ttt gta aca agc tct aac acc acg agc gct			783
Asp Leu Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Thr Thr Ser Ala			
	225	230	235
agc gca tgc gtg agc acc ggc tta aac cct aaa gcg atc aat gaa gtc			831
Ser Ala Cys Val Ser Thr Gly Leu Asn Pro Lys Ala Ile Asn Glu Val			
	240	245	250
ata ggt atc aca aaa gcc tac tcc act cgt gtg ggt aat ggg cct ttc			879

Ile	Gly	Ile	Thr	Lys	Ala	Tyr	Ser	Thr	Arg	Val	Gly	Asn	Gly	Pro	Phe		
255						260					265						
cct	agc	gaa	gac	act	aca	ccc	atg	ggc	gat	cat	tta	agg	act	aag	ggg		927
Pro	Ser	Glu	Asp	Thr	Thr	Pro	Met	Gly	Asp	His	Leu	Arg	Thr	Lys	Gly		
270					275				280						285		
gcg	gag	ttt	ggc	acg	aca	acc	aag	cgc	cca	agg	cgt	tgc	ggg	tgg	ctg		975
Ala	Glu	Phe	Gly	Thr	Thr	Thr	Lys	Arg	Pro	Arg	Arg	Cys	Gly	Trp	Leu		
				290					295					300			
gat	ttg	gtg	gct	ttg	aaa	tac	gct	tgc	gct	ttg	aat	ggg	tgc	acg	caa		1023
Asp	Leu	Val	Ala	Leu	Lys	Tyr	Ala	Cys	Ala	Leu	Asn	Gly	Cys	Thr	Gln		
			305					310					315				
tta	gcc	tta	atg	aaa	tta	gac	gtt	tta	gac	ggg	att	gat	gcg	att	aag		1071
Leu	Ala	Leu	Met	Lys	Leu	Asp	Val	Leu	Asp	Gly	Ile	Asp	Ala	Ile	Lys		
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gtg	tgc	gtg	gct	tat	gaa	aga	aag	ggc	gaa	aga	ttg	gag	att	ttc	cct		1119
Val	Cys	Val	Ala	Tyr	Glu	Arg	Lys	Gly	Glu	Arg	Leu	Glu	Ile	Phe	Pro		
	335					340					345						
agc	gat	ttg	aaa	gat	tgc	gtg	ccg	atc	tat	caa	act	ttt	aaa	ggg	tgg		1167
Ser	Asp	Leu	Lys	Asp	Cys	Val	Pro	Ile	Tyr	Gln	Thr	Phe	Lys	Gly	Trp		
	350				355					360					365		
gaa	aaa	agc	gtg	ggc	gtg	aga	aaa	tta	gac	gat	tta	gag	cca	aac	gtt		1215
Glu	Lys	Ser	Val	Gly	Val	Arg	Lys	Leu	Asp	Asp	Leu	Glu	Pro	Asn	Val		
				370					375					380			
aga	gag	tat	atc	cgt	ttt	att	gaa	aaa	gaa	gtg	ggg	gta	aaa	atc	cgc		1263
Arg	Glu	Tyr	Ile	Arg	Phe	Ile	Glu	Lys	Glu	Val	Gly	Val	Lys	Ile	Arg		
			385					390					395				
ctt	att	tct	aca	agc	cct	gaa	aga	gaa	gac	acg	att	ttt	cta				1305
Leu	Ile	Ser	Thr	Ser	Pro	Glu	Arg	Glu	Asp	Thr	Ile	Phe	Leu				
			400				405					410					
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 <212> PRT
 <213> Helicobacter pylori

<400> 292

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Lys	Ile	Val	Asp	Arg	Ile	Ala	Lys	Asp	Tyr	Asp	Phe	Val	Val	Arg	Tyr		
			20					25					30				
Gln	Gly	Gly	His	Asn	Ala	Gly	His	Thr	Ile	Val	His	Lys	Gly	Val	Lys		
		35					40					45					
His	Ser	Leu	His	Leu	Met	Pro	Ser	Gly	Val	Leu	Tyr	Pro	Lys	Cys	Lys		
	50					55					60						
Asn	Ile	Ile	Ser	Ser	Ala	Val	Val	Val	Ser	Val	Lys	Asp	Leu	Cys	Glu		
	65				70				75					80			
Glu	Ile	Ser	Ala	Phe	Glu	Asp	Leu	Glu	Asn	Arg	Leu	Phe	Val	Ser	Asp		
				85				90						95			

Arg Ala His Val Ile Leu Pro Tyr His Ala Lys Lys Asp Ala Phe Lys
 100 105 110
 Glu Lys Ser Gln Asn Ile Gly Thr Lys Lys Gly Ile Gly Pro Cys
 115 120 125
 Tyr Glu Asp Lys Met Ala Arg Ser Gly Ile Arg Met Gly Asp Leu Leu
 130 135 140
 Asp Asp Lys Ile Leu Glu Glu Lys Leu Asn Ala His Phe Lys Ala Ile
 145 150 155 160
 Glu Pro Phe Lys Lys Ala Tyr Asp Leu Gly Glu Asn Tyr Glu Lys Asp
 165 170 175
 Leu Met Gly Tyr Phe Lys Thr Tyr Ala Pro Lys Ile Cys Pro Phe Ile
 180 185 190
 Lys Asp Thr Thr Ser Met Leu Ile Glu Ala Asn Gln Lys Gly Glu Lys
 195 200 205
 Ile Leu Leu Glu Gly Ala Gln Gly Thr Leu Leu Asp Ile Asp Leu Gly
 210 215 220
 Thr Tyr Pro Phe Val Thr Ser Ser Asn Thr Thr Ser Ala Ser Ala Cys
 225 230 235 240
 Val Ser Thr Gly Leu Asn Pro Lys Ala Ile Asn Glu Val Ile Gly Ile
 245 250 255
 Thr Lys Ala Tyr Ser Thr Arg Val Gly Asn Gly Pro Phe Pro Ser Glu
 260 265 270
 Asp Thr Thr Thr Pro Met Gly Asp His Leu Arg Thr Lys Gly Ala Glu Phe
 275 280 285
 Gly Thr Thr Thr Lys Arg Pro Arg Arg Cys Gly Trp Leu Asp Leu Val
 290 295 300
 Ala Leu Lys Tyr Ala Cys Ala Leu Asn Gly Cys Thr Gln Leu Ala Leu
 305 310 315 320
 Met Lys Leu Asp Val Leu Asp Gly Ile Asp Ala Ile Lys Val Cys Val
 325 330 335
 Ala Tyr Glu Arg Lys Gly Glu Arg Leu Glu Ile Phe Pro Ser Asp Leu
 340 345 350
 Lys Asp Cys Val Pro Ile Tyr Gln Thr Phe Lys Gly Trp Glu Lys Ser
 355 360 365
 Val Gly Val Arg Lys Leu Asp Asp Leu Glu Pro Asn Val Arg Glu Tyr
 370 375 380
 Ile Arg Phe Ile Glu Lys Glu Val Gly Val Lys Ile Arg Leu Ile Ser
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 Thr Ser Pro Glu Arg Glu Asp Thr Ile Phe Leu
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 Val Leu Ser Val Ser Glu Ile Asn Ala Gln Ile Lys Ala Leu Leu Glu
 5 10 15

gcg act ttt ttg caa gtt agg gtt caa ggg gaa gtg agt aat ttg act	152
Ala Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr	
20 25 30	
atc cat aag gtg agc ggc cat gcg tat ttt tcg ctc aaa gac agc cag	200
Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln	
35 40 45 50	
tcg gtt att aaa tgc gtg ctg ttt aaa ggg aac gct aac agg ctc aaa	248
Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys	
55 60 65	
ttc gct tta aaa gaa ggg cag gaa gtg gtt gtt ttt ggg ggt att agc	296
Phe Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly Ile Ser	
70 75 80	
gtg tat gtc cca agg ggg gat tat caa atc aat tgc ttt gaa ata gag	344
Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu	
85 90 95	
cct aag gat ata ggt tca tta act tta gct tta gag caa ttg aaa gaa	392
Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu	
100 105 110	
aaa tta cgc ctt aaa ggc tat ttt gat gaa gaa aat aaa tta ccc aaa	440
Lys Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys	
115 120 125 130	
ccg cat ttt cct aaa cga gtg gca gtc atc act tct caa aat tca gcc	488
Pro His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala	
135 140 145	
gct tgg gcg gac atg aaa aag atc gct tcc aaa cga tgg ccg atg tgt	536
Ala Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys	
150 155 160	
gaa tta gtt tgt atc aac acc tta atg caa ggg gag ggc tgc gtt caa	584
Glu Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln	
165 170 175	
agc gtg gtg gaa agc atc gtt tat gcg gat agt ttt cat gac aca aaa	632
Ser Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys	
180 185 190	
aac gct ttt gat gcg att gta gtg gct agg ggt ggg ggg agc atg gag	680
Asn Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu	
195 200 205 210	
gat ttg tat tot ttc aat gat gaa aaa atc gct gat gct ctg tat ttg	728
Asp Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu	
215 220 225	
gcc aaa acc ttc agc atg tca gct att ggg cat gag agc gat ttt tta	776
Ala Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu	
230 235 240	
ttg agc gat tta gtg gcg gat tta agg gct tct acg cct tca aac gcg	824
Leu Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala	
245 250 255	

atg gaa att tta ctc ccc agc agc gat gaa tgg ttg caa aga ctt gat	872
Met Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg Leu Asp	
260 265 270	
ggg ttt aat gtg aaa ttg cac cgc tgc ttt aaa act ttg ctc cac caa	920
Gly Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln	
275 280 285 290	
aaa aag gcg cat tta gag cat tta gtg gct tct tta aaa cga ttg agt	968
Lys Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser	
295 300 305	
ttt gaa aac aag cac cat tta aac gct tta aaa cta gaa aaa tta aaa	1016
Phe Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys	
310 315 320	
atc gcc cta gaa aat aaa act cta gaa ttt tta cgc ttt aaa aaa acg	1064
Ile Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr	
325 330 335	
ctt tta gaa aaa atc tct act caa aca tta aca agc cct ttt tta caa	1112
Leu Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln	
340 345 350	
act aaa aca gag cga ttg aac agg cta gaa aac gcc ctt aaa ctc gct	1160
Thr Lys Thr Glu Arg Leu Asn Arg Leu Glu Asn Ala Leu Lys Leu Ala	
355 360 365 370	
cat gct aat ttg aaa tta ccc caa ttc ggg gcg ttg gtg agc aaa aat	1208
His Ala Asn Leu Lys Leu Pro Gln Phe Gly Ala Leu Val Ser Lys Asn	
375 380 385	
aat caa gcg ata gaa tta gag gca tta aaa agg ggc gat aaa att gaa	1256
Asn Gln Ala Ile Glu Leu Glu Ala Leu Lys Arg Gly Asp Lys Ile Glu	
390 395 400	
tta agt aat gaa aaa acc aga gcg agc gct gaa att ttg agc gtg gat	1304
Leu Ser Asn Glu Lys Thr Arg Ala Ser Ala Glu Ile Leu Ser Val Asp	
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Arg Val	
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ttc	1363
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Leu Thr Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp	
35 40 45	

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gct tat agt ttg att gaa ggc atg acg aat atc ccc tta att gca gat Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile Ala Asp 245 250 255	824
gtt ttg caa gag gga ttg cgt ggc gtc tat cat tct aga gag ata gac Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu Ile Asp 260 265 270	872
ttt gta gaa aaa gtg gtt gtt tta gac agc tgt caa atc cac caa aaa Phe Val Glu Lys Val Val Val Leu Asp Ser Cys Gln Ile His Gln Lys 275 280 285 290	920
gcg tta atg cat ttg caa gaa act ttg atg ata gaa gtg gat agg ctt Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp Arg Leu 295 300 305	968
gat ttt tct tta gtg gag cgc ttg aac att tta gcg cgc atg gag aat Asp Phe Ser Leu Val Glu Arg Leu Asn Ile Leu Ala Arg Met Glu Asn 310 315 320	1016
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Glu Thr Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu 50 55 60	
Lys Ile Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser 65 70 75 80	
Ala Met Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu 85 90 95	
Gln Ile Lys Gln Glu Asn Gln Asp Tyr His Ala Cys Glu Val Asn Gln 100 105 110	
Lys Tyr Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys 115 120 125	
Arg Phe Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu 130 135 140	
Ile Tyr Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr 145 150 155 160	
Leu Leu Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys 165 170 175	

agt ttg agc gat aat gtc aaa ttg caa gaa gat ggg atc gtt ttt aaa	396
Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe Lys	
100 105 110	
tcc cat att gat ggg agc aag cat cta ttc acg ccc gct aaa gtt ttg	444
Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val Leu	
115 120 125	
gac att caa tat tct ttg aat agc gat att atg atg gtt tta gac gat	492
Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp Asp	
130 135 140 145	
tta gtg ggc ttg ccc gct ccc tta aaa cgc ctt gaa gaa tcc att aaa	540
Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile Lys	
150 155 160	
aga agt gct aaa tgg gcg aat atg agc cta gaa tac cac aaa gaa aaa	588
Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu Lys	
165 170 175	
aac cgc ccg agc aac aac ctt ttt gcc att atc cag ggc ggg acg cat	636
Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr His	
180 185 190	
ttg aaa atg cgc agc ctt agc gtg gga tta acg cat gag ggt ttt gat	684
Leu Lys Met Arg Ser Leu Ser Val Gly Leu Thr His Glu Gly Phe Asp	
195 200 205	
ggc tac gct ata ggc ggt tta gcg gtg ggg gaa agc gct gat gaa atg	732
Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu Met	
210 215 220 225	
cta gaa acc atc gcg cac acc gcc ccc ttg ctc ccc aaa gac aag cct	780
Leu Glu Thr Ile Ala His Thr Ala Pro Leu Leu Pro Lys Asp Lys Pro	
230 235 240	
cgc tac tta atg ggc gta ggc acg cct gaa aat atc cta gac gct atc	828
Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala Ile	
245 250 255	
agt ttg ggg gtg gat atg ttt gat tgc gtg atg ccc acc aga aac gcc	876
Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn Ala	
260 265 270	
aga aac gcc acc ctt ttc acg cat tct ggc aaa att tct atc aaa aac	924
Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys Asn	
275 280 285	
gcg ccc tat aaa ttg gat aat acc cct att gaa gaa aat tgc gca tgt	972
Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala Cys	
290 295 300 305	
tat gct tgc aaa cgc tat tct aaa gcc tat ttg cac cat tta ttt agg	1020
Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe Arg	
310 315 320	
gct aaa gaa ctc act tac gct cgt ttg gcc agc ttg cac aat ttg cat	1068
Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu His	
325 330 335	

ttt tat tta gag ctg gtg aag aac gcc aga aac gcc att tta gaa aag 1116
 Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu Lys
 340 345 350
 cgg ttt ttg agt ttt aaa aaa gaa ttt ttg gag aaa tac aac tcc cgc 1164
 Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser Arg
 355 360 365
 tct cat tgaatgatgg aatgcaaaaa tactaaaaag cgtttttttac catcaataaa 1220
 Ser His
 370
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 <213> Helicobacter pylori

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 20 25 30
 Gly Thr Gln Gly Cys Ile Lys Ser Leu Asp Ala Thr Asp Ala Gln Glu
 35 40 45
 Ile Leu Gly Ala Lys Leu Ile Leu Ala Asn Thr Tyr His Met Tyr Leu
 50 55 60
 Arg Pro Gly Glu Lys Val Val Glu Glu Leu Gly Gly Leu His Arg Phe
 65 70 75 80
 Ala Gln Phe Tyr Gly Ser Phe Leu Thr Asp Ser Gly Gly Phe Gln Ala
 85 90 95
 Phe Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe
 100 105 110
 Lys Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val
 115 120 125
 Leu Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp
 130 135 140
 Asp Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile
 145 150 155 160
 Lys Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu
 165 170 175
 Lys Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr
 180 185 190
 His Leu Lys Met Arg Ser Leu Ser Val Gly Leu Thr His Glu Gly Phe
 195 200 205
 Asp Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu
 210 215 220
 Met Leu Glu Thr Ile Ala His Thr Ala Pro Leu Leu Pro Lys Asp Lys
 225 230 235 240
 Pro Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala
 245 250 255
 Ile Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn
 260 265 270
 Ala Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys
 275 280 285
 Asn Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala
 290 295 300

Cys Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe
 305 310 315 320
 Arg Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu
 325 330 335
 His Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu
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 Lys Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser
 355 360 365
 Arg Ser His
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 Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg Thr Asn Leu Phe Asp Thr
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 caa gtg atg agc gag aat ttg aag gac ttt agc acg acc tta gaa gaa 152
 Gln Val Met Ser Glu Asn Leu Lys Asp Phe Ser Thr Thr Leu Glu Glu
 20 25 30
 caa gaa gcc gat att att atc atc aat tct tgc acc gtg acc aat ggg 200
 Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr Asn Gly
 35 40 45 50
 gcc gat agc gcg gta agg agt tac gct aaa aaa atg gca cgg ttg gat 248
 Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg Leu Asp
 55 60 65
 aag gaa gtg cta ttt act ggt tgc ggg gtg aaa acc caa ggc aaa gag 296
 Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly Lys Glu
 70 75 80
 ctt ttt gaa aaa ggg ttt tta aag ggc gtt ttt ggg cat gac aat aaa 344
 Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp Asn Lys
 85 90 95
 gaa aag att aac gcg ctt tta caa gaa aaa aag cgt ttt ttt ata gat 392
 Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe Ile Asp
 100 105 110
 gac aat tta gaa aac aag cac tta gac acc acg atg gtg agc gag ttt 440
 Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser Glu Phe
 115 120 125 130
 gtg gga aaa act agg gcg ttt att aag atc caa gaa ggc tgt gat ttt 488
 Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys Asp Phe


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115                120                125                130
caa agc gaa tgg ttg ttt aag gaa ttg ttt gtg ctg gtg tgc gct ttg      488
Gln Ser Glu Trp Leu Phe Lys Glu Leu Phe Val Leu Val Cys Ala Leu
                135                140                145

ttt ttt tgg cgt ttg ctt gga aaa aat gtg ctt tagtcccttt gatttaatca      541
Phe Phe Trp Arg Leu Leu Gly Lys Asn Val Leu
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aatgagagag tttttggcta ctatctagga aat      574

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<212> PRT
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 20          25          30
Lys Ala Ser Ser Val Leu Pro Glu Leu His Leu Thr Pro Phe Glu Ser
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Gly Lys Leu Met Ala Gln Ile Phe Val Arg Phe Asn Tyr Val Leu Gly
 50          55          60
Ala Ile Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr
 65          70          75          80
Tyr Lys Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala
 85          90          95
Leu Cys Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala
100          105          110
Gln Lys Ala Gly Glu Ala Ala Leu Gln Ser Ala Glu Phe Ala Arg Ser
115          120          125
His Ala Gln Ser Glu Trp Leu Phe Lys Glu Leu Phe Val Leu Val Cys
130          135          140
Ala Leu Phe Phe Trp Arg Leu Leu Gly Lys Asn Val Leu
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Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr Ala Thr
 5          10          15

aat ctt aat gag ctt aaa aac gcc ctg gat ttc atc tct caa aat agg      152
Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln Asn Arg

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20	25	30	
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ttt tta gat gaa aat ttt caa agc caa acc cct ttt ttg tat ttt gaa Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr Phe Glu 55 60 65			248
caa ttt tta gaa aga aaa aaa tat tct tta gag cct tta aaa gag cat Gln Phe Leu Glu Arg Lys Lys Tyr Ser Leu Glu Pro Leu Lys Glu His 70 75 80			296
gcg ttt tac cct aaa atc cat agt tct tta gat caa aaa act tat ttc Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr Tyr Phe 85 90 95			344
aag cag ttt aaa gcc gtt aaa gag cgt ctc aaa aac gcc gac acc tat Lys Gln Phe Lys Ala Val Lys Glu Arg Leu Lys Asn Gly Asp Thr Tyr 100 105 110			392
caa gtg aat ctc aca atg gat tta ttt tta gac act aaa gcc aaa cca Gln Val Asn Leu Thr Met Asp Leu Phe Leu Asp Thr Lys Ala Lys Pro 115 120 125 130			440
aag cgc gtt ttt aag gag gtg gta cac aac caa aac acg cct ttt aag Lys Arg Val Phe Lys Glu Val Val His Asn Gln Asn Thr Pro Phe Lys 135 140 145			488
gct ttt ata gaa aat gag ttt ggg agc gtt tta agc ttt tcg ccg gaa Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser Pro Glu 150 155 160			536
ttg ttt ttt gaa tta gag ttt tta gat aca gcg att aag att att aca Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile Ile Thr 165 170 175			584
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gaa aaa aac cga ttg ttt ttg caa aat gat gac aaa aac aga agc gaa Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg Ser Glu 195 200 205 210			680
aat gtg atg att gtg gat tta ttg cgt aac gat ttg agc cgc ttg gcc Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg Leu Ala 215 220 225			728
tta aaa aat agc gtg aaa gtc aat caa ttg ttt gaa atc atc agc ttg Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile Ser Leu 230 235 240			776
cct agc gtg tat caa atg ata agc gag att gaa gcg aaa ttg ccc cta Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Lys Leu Pro Leu 245 250 255			824
aaa acc agc ttg ttt gag att ttt aag gcg ttg ttc cct tgc gcc tct			872

Lys Thr Ser Leu Phe Glu Ile Phe Lys Ala Leu Phe Pro Cys Gly Ser	
260 265 270	
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Val Thr Gly Cys Pro Lys Ile Lys Thr Met Gln Ile Ile Glu Ser Leu	
275 280 285 290	
gaa aaa cgc cct agg ggg gtg tat tgc ggg gcg ata ggc atg gtt gaa	968
Glu Lys Arg Pro Arg Gly Val Tyr Cys Gly Ala Ile Gly Met Val Glu	
295 300 305	
gaa aaa aaa gcc ctt ttt agc gtg cct atc cgc act tta gaa aaa aga	1016
Glu Lys Lys Ala Leu Phe Ser Val Pro Ile Arg Thr Leu Glu Lys Arg	
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Val His Glu Asn Phe Leu His Leu Gly Val Gly Ser Gly Val Thr Tyr	
325 330 335	
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Lys Ser Lys Ala Pro Lys Glu Tyr Glu Glu Ser Phe Leu Lys Ser Phe	
340 345 350	
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Phe Val Met Pro Lys Ile Glu Phe Glu Ile Val Glu Thr Met Lys Ile	
355 360 365 370	
atc aaa aag gat caa aaa tta gag att aat aat aaa aac gcc cat aaa	1208
Ile Lys Lys Asp Gln Lys Leu Glu Ile Asn Asn Lys Asn Ala His Lys	
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Glu Arg Leu Met Asn Ser Thr Arg Tyr Phe Asn Phe Lys Tyr Asp Glu	
390 395 400	
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Asn Leu Leu Asp Phe Glu Leu Glu Lys Glu Gly Val Leu Arg Val Leu	
405 410 415	
ctc aat aaa aag ggc aag ctc att aaa gaa tac aaa acc tta gag cct	1352
Leu Asn Lys Lys Gly Lys Leu Ile Lys Glu Tyr Lys Thr Leu Glu Pro	
420 425 430	
tta aaa agc cta gaa atc cgt ttg agt gaa gcc ccc att gat aaa cgc	1400
Leu Lys Ser Leu Glu Ile Arg Leu Ser Glu Ala Pro Ile Asp Lys Arg	
435 440 445 450	
aat gat ttt tta tac cat aag acc act tat gcc cct ttt tat caa aag	1448
Asn Asp Phe Leu Tyr His Lys Thr Thr Tyr Ala Pro Phe Tyr Gln Lys	
455 460 465	
gct cga gcg ctc att aaa aag ggc gtt atg ttt gat gaa atc ttt tat	1496
Ala Arg Ala Leu Ile Lys Lys Gly Val Met Phe Asp Glu Ile Phe Tyr	
470 475 480	
aac cag gat ttg gaa ctc act gag ggc gct agg agc aat ctt gtt tta	1544
Asn Gln Asp Leu Glu Leu Thr Glu Gly Ala Arg Ser Asn Leu Val Leu	
485 490 495	

	275		280		285
Ser	Leu	Glu	Lys	Arg	Pro
290				Arg	Gly
Val	Glu	Glu	Lys	Lys	Ala
305				310	Leu
Lys	Arg	Val	His	Glu	Asn
				325	Phe
Thr	Tyr	Lys	Ser	Lys	Ala
				340	Pro
Ser	Phe	Phe	Val	Met	Pro
				355	Lys
Lys	Ile	Ile	Lys	Lys	Asp
370				375	Gln
His	Lys	Glu	Arg	Leu	Met
385				390	Asn
Asp	Glu	Asn	Leu	Leu	Asp
				405	Phe
Val	Leu	Leu	Asn	Lys	Lys
				420	Gly
Glu	Pro	Leu	Lys	Ser	Leu
				435	Glu
Lys	Arg	Asn	Asp	Phe	Leu
				450	Tyr
Gln	Lys	Ala	Arg	Ala	Leu
465				470	Ile
Phe	Tyr	Asn	Gln	Asp	Leu
				485	Glu
Val	Leu	Glu	Ile	His	Asn
				500	Arg
Ala	Leu	Asn	Gly	Thr	Gly
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Gly	His	Ala	Pro	Leu	Lys
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545				550	Tyr

<210> 305
 <211> 958
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (51)...(905)

<400> 305

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tct ttt aga gag ttt atc caa caa ttc aaa aaa aat aag gca gcg gtc	104
Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala Ala Val	
5 10 15	
gtt ggg gct tgg att gtg ctt tta ttg gta att tgc gcg att ttt gcg	152
Val Gly Ala Trp Ile Val Leu Leu Val Ile Cys Ala Ile Phe Ala	
20 25 30	
ccc ctt tta gcc ccg cat gat cct tat gtc caa aac gcg caa gat cgc	200

Pro 35	Leu	Leu	Ala	Pro	His 40	Asp	Pro	Tyr	Val	Gln 45	Asn	Ala	Gln	Asp	Arg 50	
ctt	ttg	aag	cct	ata	ttg	gag	cat	gga	ggg	aat	gct	aaa	tac	ctt	tta	248
Leu	Leu	Lys	Pro	Ile	Trp	Glu	His	Gly	Gly	Asn	Ala	Lys	Tyr	Leu	Leu	
				55					60					65		
ggc	acc	gat	gat	ttg	ggg	cgc	gat	att	ttg	agc	cgc	ttg	atc	tat	ggg	296
Gly	Thr	Asp	Asp	Leu	Gly	Arg	Asp	Ile	Leu	Ser	Arg	Leu	Ile	Tyr	Gly	
			70					75					80			
gcc	agg	att	tct	tta	acc	ata	ggg	att	gtt	tct	atg	ggg	att	gcg	gtg	344
Ala	Arg	Ile	Ser	Leu	Thr	Ile	Gly	Ile	Val	Ser	Met	Gly	Ile	Ala	Val	
		85					90					95				
ttt	ttt	ggc	acg	ata	cta	ggg	cta	ata	gcg	ggg	tat	ttt	ggg	ggg	aaa	392
Phe	Phe	Gly	Thr	Ile	Leu	Gly	Leu	Ile	Ala	Gly	Tyr	Phe	Gly	Gly	Lys	
	100					105					110					
aca	gat	gca	att	atc	atg	cgt	atc	atg	gac	atc	atg	ttc	gct	ttg	ccc	440
Thr	Asp	Ala	Ile	Ile	Met	Arg	Ile	Met	Asp	Ile	Met	Phe	Ala	Leu	Pro	
115					120					125					130	
tct	att	tta	ttg	atc	gtg	att	gtg	gtc	gcg	gtg	tta	ggg	cct	tca	ctc	488
Ser	Ile	Leu	Leu	Ile	Val	Ile	Val	Val	Ala	Val	Leu	Gly	Pro	Ser	Leu	
				135					140					145		
act	aac	gcc	atg	ctc	gct	att	ggg	ttt	gtg	ggg	att	cct	ggg	ttt	gca	536
Thr	Asn	Ala	Met	Leu	Ala	Ile	Gly	Phe	Val	Gly	Ile	Pro	Gly	Phe	Ala	
		150						155					160			
aga	ttg	gtg	cgc	agt	tcc	gtg	cta	ggg	gaa	aaa	gaa	aaa	gaa	tac	gtg	584
Arg	Leu	Val	Arg	Ser	Ser	Val	Leu	Gly	Glu	Lys	Glu	Lys	Glu	Tyr	Val	
		165				170						175				
atc	gct	tct	aaa	atc	aat	ggc	tct	tcg	cat	ctt	cgt	ttg	atg	tgt	aag	632
Ile	Ala	Ser	Lys	Ile	Asn	Gly	Ser	Ser	His	Leu	Arg	Leu	Met	Cys	Lys	
	180					185					190					
gtg	att	ttc	cct	aat	tgc	att	atc	cct	tta	atc	gtt	caa	acg	aca	atg	680
Val	Ile	Phe	Pro	Asn	Cys	Ile	Ile	Pro	Leu	Ile	Val	Gln	Thr	Thr	Met	
195				200						205					210	
ggg	ttt	gct	tcc	acg	gtt	tta	gaa	gcg	gct	gca	ctg	agc	ttc	tta	ggg	728
Gly	Phe	Ala	Ser	Thr	Val	Leu	Glu	Ala	Ala	Ala	Leu	Ser	Phe	Leu	Gly	
				215					220					225		
ctt	ggg	gcc	caa	cct	ccc	aaa	ccc	gaa	ttg	gga	gcg	atg	ttg	atg	aat	776
Leu	Gly	Ala	Gln	Pro	Pro	Lys	Pro	Glu	Trp	Gly	Ala	Met	Leu	Met	Asn	
			230					235						240		
tcc	atg	caa	tac	atc	gct	acc	gct	cct	ttg	atg	ctt	gtt	ttc	cct	ggg	824
Ser	Met	Gln	Tyr	Ile	Ala	Thr	Ala	Pro	Trp	Met	Leu	Val	Phe	Pro	Gly	
		245			</											

atc atg gac gct tta gat cct aaa cgc acc tct taaaaggagc ttgcatgatt 925
 Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser
 275 280 285

ttagaagtta aagatttaaa aacttatttt ttc 958

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 <212> PRT
 <213> Helicobacter pylori

<400> 306
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 Phe Ala Pro Leu Leu Ala Pro His Asp Pro Tyr Val Gln Asn Ala Gln
 35 40 45
 Asp Arg Leu Leu Lys Pro Ile Trp Glu His Gly Gly Asn Ala Lys Tyr
 50 55 60
 Leu Leu Gly Thr Asp Asp Leu Gly Arg Asp Ile Leu Ser Arg Leu Ile
 65 70 75 80
 Tyr Gly Ala Arg Ile Ser Leu Thr Ile Gly Ile Val Ser Met Gly Ile
 85 90 95
 Ala Val Phe Phe Gly Thr Ile Leu Gly Leu Ile Ala Gly Tyr Phe Gly
 100 105 110
 Gly Lys Thr Asp Ala Ile Ile Met Arg Ile Met Asp Ile Met Phe Ala
 115 120 125
 Leu Pro Ser Ile Leu Leu Ile Val Ile Val Val Ala Val Leu Gly Pro
 130 135 140
 Ser Leu Thr Asn Ala Met Leu Ala Ile Gly Phe Val Gly Ile Pro Gly
 145 150 155 160
 Phe Ala Arg Leu Val Arg Ser Ser Val Leu Gly Glu Lys Glu Lys Glu
 165 170 175
 Tyr Val Ile Ala Ser Lys Ile Asn Gly Ser Ser His Leu Arg Leu Met
 180 185 190
 Cys Lys Val Ile Phe Pro Asn Cys Ile Ile Pro Leu Ile Val Gln Thr
 195 200 205
 Thr Met Gly Phe Ala Ser Thr Val Leu Glu Ala Ala Ala Leu Ser Phe
 210 215 220
 Leu Gly Leu Gly Ala Gln Pro Pro Lys Pro Glu Trp Gly Ala Met Leu
 225 230 235 240
 Met Asn Ser Met Gln Tyr Ile Ala Thr Ala Pro Trp Met Leu Val Phe
 245 250 255
 Pro Gly Val Met Ile Phe Leu Thr Val Met Ser Phe Asn Leu Val Gly
 260 265 270
 Asp Gly Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser
 275 280 285

<210> 307
 <211> 791
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (95)...(727)

<400> 307

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aaagcgc	cagc	nctt	tctt	gga	caaaaa	attt	gtat	atg	gga	gtc	aat	tac	caa	aca		115
								Met	Gly	Val	Asn	Tyr	Gln	Thr		
								1				5				
gg	t	a	a	t	a	a	t	a	c	a	a	a	a	a	a	163
Gly	Ser	Ile	Asn	Leu	Met	Thr	Asn	Ile	His	Glu	Val	Arg	Glu	Val	Thr	
		10					15					20				
aac	tat	caa	acc	gg	tac	acc	aat	att	ata	act	agc	g	aat	agc	g	211
Asn	Tyr	Gln	Thr	Gly	Tyr	Thr	Asn	Ile	Ile	Thr	Ser	Val	Asn	Ser	Val	
	25					30					35					
aaa	aag	ctc	acc	aac	atg	gga	tct	aat	ggg	att	gga	tta	gtc	atg	gg	259
Lys	Lys	Leu	Thr	Asn	Met	Gly	Ser	Asn	Gly	Ile	Gly	Leu	Val	Met	Gly	
40					45				50						55	
tat	aac	cac	ttt	ttc	cat	ccg	gat	aaa	atc	ttg	ggc	ttg	cgc	tat	ttc	307
Tyr	Asn	His	Phe	Phe	His	Pro	Asp	Lys	Ile	Leu	Gly	Leu	Arg	Tyr	Phe	
				60					65					70		
gct	ttt	tta	gat	tgg	caa	ggc	tat	ggc	atg	aga	tac	cct	aaa	ggc	tat	355
Ala	Phe	Leu	Asp	Trp	Gln	Gly	Tyr	Gly	Met	Arg	Tyr	Pro	Lys	Gly	Tyr	
			75				80						85			
tat	ggc	ggc	aat	aac	atg	atc	act	tat	ggc	gtg	ggc	gtg	gat	gca	gtg	403
Tyr	Gly	Gly	Asn	Asn	Met	Ile	Thr	Tyr	Gly	Val	Gly	Val	Asp	Ala	Val	
		90					95					100				
tgg	aat	ttc	ttt	caa	ggg	agt	ttc	tat	caa	gat	gac	att	agc	gtg	gat	451
Trp	Asn	Phe	Phe	Gln	Gly	Ser	Phe	Tyr	Gln	Asp	Asp	Ile	Ser	Val	Asp	
	105					110					115					
att	ggc	g	ttt	ggg	ggg	att	gcg	att	gcg	ggg	aat	agc	tgg	tat	att	499
Ile	Gly	Val	Phe	Gly	Gly	Ile	Ala	Ile	Ala	Gly	Asn	Ser	Trp	Tyr	Ile	
120					125					130					135	
ggc	agt	aaa	ggg	cag	gaa	ttg	tta	gg	atc	act	aac	agc	agc	gcg	gtt	547
Gly	Ser	Lys	Gly	Gln	Glu	Leu	Leu	Gly	Ile	Thr	Asn	Ser	Ser	Ala	Val	
				140					145					150		
gat	aac	acc	tct	ttt	caa	ttc	ctc	ttt	aac	ttt	ggc	ctc	aag	gct	tta	595
Asp	Asn	Thr	Ser	Phe	Gln	Phe	Leu	Phe	Asn	Phe	Gly	Leu	Lys	Ala	Leu	
			155					160					165			
ttt	gta	gat	gag	cat	gaa	ttt	gaa	atc	gg	ttt	aaa	ttc	ccc	acc	att	643
Phe	Val	Asp	Glu	His	Glu	Phe	Glu	Ile	Gly	Phe	Lys	Phe	Pro	Thr	Ile	
		170					175					180				
aat	aac	aaa	tac	tac	acc	act	gac	gcg	ctc	aag	gtt	caa	atg	cgt	agg	691
Asn	Asn	Lys	Tyr	Tyr	Thr	Thr	Asp	Ala	Leu	Lys	Val	Gln	Met	Arg	Arg	
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gtc	ttt	gcc	ttt	tat												

<210> 308
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 <212> PRT
 <213> Helicobacter pylori

<400> 308
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 20 25 30
 Ile Thr Ser Val Asn Ser Val Lys Lys Leu Thr Asn Met Gly Ser Asn
 35 40 45
 Gly Ile Gly Leu Val Met Gly Tyr Asn His Phe Phe His Pro Asp Lys
 50 55 60
 Ile Leu Gly Leu Arg Tyr Phe Ala Phe Leu Asp Trp Gln Gly Tyr Gly
 65 70 75 80
 Met Arg Tyr Pro Lys Gly Tyr Tyr Gly Gly Asn Asn Met Ile Thr Tyr
 85 90 95
 Gly Val Gly Val Asp Ala Val Trp Asn Phe Phe Gln Gly Ser Phe Tyr
 100 105 110
 Gln Asp Asp Ile Ser Val Asp Ile Gly Val Phe Gly Gly Ile Ala Ile
 115 120 125
 Ala Gly Asn Ser Trp Tyr Ile Gly Ser Lys Gly Gln Glu Leu Leu Gly
 130 135 140
 Ile Thr Asn Ser Ser Ala Val Asp Asn Thr Ser Phe Gln Phe Leu Phe
 145 150 155 160
 Asn Phe Gly Leu Lys Ala Leu Phe Val Asp Glu His Glu Phe Glu Ile
 165 170 175
 Gly Phe Lys Phe Pro Thr Ile Asn Asn Lys Tyr Tyr Thr Thr Asp Ala
 180 185 190
 Leu Lys Val Gln Met Arg Arg Val Phe Ala Phe Tyr Val Gly Tyr Asn
 195 200 205
 Tyr His Phe
 210

<210> 309
 <211> 517
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (51)...(464)

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 ggg ggt gga acg gta aaa aaa gac ttg aag aaa gcc att caa tac tat 104
 Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr
 5 10 15
 gtt aaa gcg tgt gaa ttg aat gaa atg ttt ggg tgt ctg tca tta gtt 152
 Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val
 20 25 30
 tcg aac tct caa ata aac aaa caa aaa ctc ttt caa tat ctc tct aaa 200
 Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys

<221> CDS
 <222> (51)...(398)

<400> 311

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gtggaacgct ctgtcttagc aaattgatct tagcggcgctc gtttttgata gtg gat      56
                                   Val Asp
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tca gag ggg ttt tcg cct tct att tat acc gac aag aca ggg cat ccc      104
Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly His Pro
      5                                10                                15

acg att ggc tat ggc tat aat ttg agc gtt tat tct tat gag ggt aag      152
Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu Gly Lys
      20                                25                                30

cgt atc acc aaa aca tat ggg ctt tta act gac ata ctc tct tat ggg      200
Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser Tyr Gly
      35                                40                                45                                50

tgg tat aaa aat ttg gac gca atg agg aga atg gtc atc ttg gat ttg      248
Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu Asp Leu
      55                                60                                65

agc tac aat tta ggc ttg aac gga ctg ctc aaa ttc aag caa ttc atc      296
Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln Phe Ile
      70                                75                                80

aag gcc ata gag gat aaa aat tat gct ttg gct gtg gag aga ctg caa      344
Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg Leu Gln
      85                                90                                95

aaa agc ccg tat ttc aat caa gtg aaa aaa gag cgt caa gga ata tgg      392
Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly Ile Trp
      100                                105                                110

aaa ttt tgaaattgga gggttgcgaa aaacattgta agaaaaaata cgcaatagaa      448
Lys Phe
115

aag                                                                    451
  
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<210> 312
 <211> 116
 <212> PRT
 <213> Helicobacter pylori

<400> 312

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Val Asp Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly
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His Pro Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu
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Gly Lys Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser
      35                                40                                45
Tyr Gly Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu
      50                                55                                60
Asp Leu Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln
      65                                70                                75                                80
Phe Ile Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg
  
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Leu Gln Lys Ser 85 Pro Tyr Phe Asn Gln 90 Val Lys Lys Glu Arg 95 Gln Gly
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 Ile Trp Lys Phe
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<210> 313
 <211> 399
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (50)...(346)

<400> 313
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 Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg Ile Phe Ile
 5 10 15

cac cag cat gag aat aaa aat cag aat att gac tat gag caa cca aac 154
 His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu Gln Pro Asn
 20 25 30 35

gat aga agc aaa ttc cac gct cac cct ttc aag agc gtt tta aca acc 202
 Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val Leu Thr Thr
 40 45 50

caa acg cta cca ctt ggt ttt tta gag aga gaa aga gag aga aag caa 250
 Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu Arg Lys Gln
 55 60 65

aat ttt aag att gat tct caa atc tat tcc ttt gca aaa gtt aag att 298
 Asn Phe Lys Ile Asp Ser Gln Ile Tyr Ser Phe Ala Lys Val Lys Ile
 70 75 80

ggg tgt ttt aac atg att ttt ggc ctg ctc gca tca agc cct tat ttt 346
 Gly Cys Phe Asn Met Ile Phe Gly Leu Leu Ala Ser Ser Pro Tyr Phe
 85 90 95

taacatttcc gctcccttgc ttttttaaag cctccctaaa ttactacacc act 399

<210> 314
 <211> 99
 <212> PRT
 <213> Helicobacter pylori

<400> 314
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 Ile Phe Ile His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu
 20 25 30
 Gln Pro Asn Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val
 35 40 45
 Leu Thr Thr Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu

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 Ser Leu Lys Met His Gln Arg Lys Cys Phe Ala Lys Cys Phe Val Asn
 50 55 60
 Ser Glu Ser Phe Leu Ser Lys Met Leu His Ser Pro Ile Met Val Ile
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 Cys Phe Tyr Phe Ile Phe Ser Ile Phe Thr Ser Ile Ser Ile Val Tyr
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 Ser Val Leu Asp Tyr Asp Gln Met Met Trp Gly Phe Val Phe Cys Thr
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 Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp Lys Leu
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 Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala Glu Gln
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 His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe Lys Pro
 35 40 45 50
 ttt gtg agc atc tat tct act ttt ttg cag agg gct tat gat tct att 248
 Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Ser Ile
 55 60 65
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 Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala Ile Asp
 70 75 80

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Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe Ala Pro	
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Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe Ala Leu	
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Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln Ser Glu	
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Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp Pro Asn	
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Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe Leu Ser	
230 235 240	
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Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile Asp Glu	
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 Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp
 50 55 60
 Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala
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 115 120 125
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 Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe
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 Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu
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 Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr Ala Arg
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gaa aaa aat aag agc gag atc tat aat gtc ggc tac aat caa ggc cat	872
Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln Gly His	
260 265 270	
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Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn Asn Asp	
275 280 285 290	
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Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala Ser Leu	
295 300 305	
att gcc aat aac gct aaa atc tta caa aac acc tct ttc aaa ccc ctt	1016
Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys Pro Leu	
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Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp Glu Glu	
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Tyr Pro Asn Arg Val Val Phe Ile Gln Ala Asn Leu Asn Glu Thr His	
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130 135 140	
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			180					185					190		
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Phe	Gly	Asp	Thr	Gly	Ser	Gly	Lys	Thr	Glu	Ile	Tyr	Met	His	Ala	Ile						
				135					140					145							
gcc	caa	act	tta	gag	caa	aaa	aaa	agc	gct	tta	ttg	ttg	gtg	cca	gaa						536
Ala	Gln	Thr	Leu	Glu	Gln	Lys	Lys	Ser	Ala	Leu	Leu	Leu	Val	Pro	Glu						
			150					155					160								
atc	gct	ctc	acc	cct	caa	atg	caa	caa	cgc	ctt	aaa	agg	gtt	ttt	aaa						584
Ile	Ala	Leu	Thr	Pro	Gln	Met	Gln	Gln	Arg	Leu	Lys	Arg	Val	Phe	Lys						
			165				170					175									
gaa	aat	tta	ggc	ttg	tgg	cat	agc	aaa	ctc	tct	caa	aat	caa	aaa	aaa						632
Glu	Asn	Leu	Gly	Leu	Trp	His	Ser	Lys	Leu	Ser	Gln	Asn	Gln	Lys	Lys						
	180					185					190										
caa	ttt	tta	gaa	aag	ctt	tat	tcg	caa	gaa	atc	aaa	tta	gtg	gta	ggc						680
Gln	Phe	Leu	Glu	Lys	Leu	Tyr	Ser	Gln	Glu	Ile	Lys	Leu	Val	Val	Gly						
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aca	cga	agc	gcg	ttg	ttt	tta	ccc	ctt	aaa	gag	ctg	ggg	tta	atc	att						728
Thr	Arg	Ser	Ala	Leu	Phe	Leu	Pro	Leu	Lys	Glu	Leu	Gly	Leu	Ile	Ile						
				215					220					225							
gta	gat	gaa	gag	cat	gac	ttt	tct	tat	aaa	tcc	cat	caa	agc	cct	atg						776
Val	Asp	Glu	Glu	His	Asp	Phe	Ser	Tyr	Lys	Ser	His	Gln	Ser	Pro	Met						
			230					235					240								
tat	aac	gct	agg	gat	tta	tgc	ttg	tat	tta	tct	cat	aaa	ttc	cct	att						824
Tyr	Asn	Ala	Arg	Asp	Leu	Cys	Leu	Tyr	Leu	Ser	His	Lys	Phe	Pro	Ile						
		245					250					255									
caa	gtg	atc	tta	ggc	tct	gct	acg	cca	agt	ttg	aat	agt	tat	aaa	cgc						872
Gln	Val	Ile	Leu	Gly	Ser	Ala	Thr	Pro	Ser	Leu	Asn	Ser	Tyr	Lys	Arg						
	260					265					270										
ttt	aaa	gat	aag	gct	tta	gtg	cgc	tta	aag	ggg	cgc	tac	acc	ccc	acg						920
Phe	Lys	Asp	Lys	Ala	Leu	Val	Arg	Leu	Lys	Gly	Arg	Tyr	Thr	Pro	Thr						
275				280					285					290							
caa	aaa	aac	att	att	ttt	gaa	aaa	acc	gag	cgt	ttt	atc	acg	ccc	aaa						968
Gln	Lys	Asn	Ile																		

Cys 340	Tyr	Lys	Ser	Val	Gln	Cys 345	Pro	Phe	Cys	Ser	Val 350	Asn	Met	Ser	Leu	
cat His 355	tta Leu	aag Lys	acc Thr	aac Asn	aaa Lys 360	ctc Leu	atg Met	tgc Cys	cat His 365	tat Tyr	tgc Cys	cat His	ttt Phe	tca Ser	agc Ser 370	1160
cct Pro	atc Ile	cct Pro	aaa Lys	att Ile 375	tgc Cys	agc Ser	gcg Ala	tgt Cys	caa Gln 380	agc Ser	gaa Glu	gtc Val	tta Leu	gtg Val 385	ggc Gly	1208
aaa Lys	agg Arg	ata Ile	ggc Gly 390	act Thr	atg Met	caa Gln	gtg Val	cta Leu 395	aag Lys	gaa Glu	tta Leu	gag Glu	agc Ser 400	ctt Leu	tta Leu	1256
gag Glu	ggg Gly	gct Ala 405	aaa Lys	ata Ile	gcg Ala	att Ile	tta Leu 410	gat Asp	aaa Lys	gat Asp	cac His	act Thr 415	agc Ser	acg Thr	caa Gln	1304
aaa Lys 420	aaa Lys	ctc Leu	cac His	aat Asn	att Ile	tta Leu 425	aac Asn	gat Asp	ttc Phe	aac Asn	gct Ala 430	caa Gln	aaa Lys	acg Thr	aat Asn	1352
atc Ile 435	tta Leu	atc Ile	ggc Gly	act Thr	caa Gln 440	atg Met	ata Ile	agc Ser	aaa Lys 445	ggg Gly	cat His	gat Asp	tac Tyr	gct Ala	aaa Lys 450	1400
gtg Val	agt Ser	ttg Leu	gcg Ala	gtt Val 455	gtt Val	tta Leu	ggc Gly	ata Ile	gac Asp 460	aat Asn	atc Ile	atc Ile	aaa Lys	tct Ser 465	aat Asn	1448
agt Ser	tat Tyr	agg Arg	gct Ala 470	tta Leu	gaa Glu	gaa Glu	ggc Gly	gtg Val 475	tcg Ser	tta Leu	ctt Leu	tat Tyr	caa Gln 480	atc Ile	gct Ala	1496
ggg Gly	agg Arg	agc Ser 485	gct Ala	agg Arg	caa Gln	att Ile	tct Ser 490	ggc Gly	caa Gln	gtg Val	ttc Phe	att Ile 495	caa Gln	agc Ser	acc Thr	1544
gaa Glu 500	acc Thr	gat Asp	ctg Leu	tta Leu	gaa Glu	aat Asn 505	ttc Phe	tta Leu	gaa Glu	gat Asp	tat Tyr 510	gaa Glu	gat Asp	ttt Phe	tta Leu	1592
caa Gln 515	tac Tyr	gaa Glu	ttg Leu	caa Gln	gaa Glu 520	agg Arg	tgc Cys	gaa Glu	ctc Leu	tac Tyr 525	ccg Pro	cct Pro	ttt Phe	tct Ser	agg Arg 530	1640
ctg Leu	tgt Cys	ttg Leu	ttg Leu	gag Glu 535	ttt Phe	aag Lys	cat His	aaa Lys	aac Asn 540	gaa Glu	gaa Glu	aaa Lys	gcc Ala	caa Gln 545	caa Gln	1688
ttg Leu	agc Ser	cta Leu	aaa Lys 550	gcc Ala	tct Ser	caa Gln	acc Thr	ctt Leu 555	tct Ser	tcg Ser	tgt Cys	tta Leu	gaa Glu 560	aag Lys	ggc Gly	1736
gta Val	acg Thr	ctc Leu 565	tct Ser	aat Asn	ttc Phe	aaa Lys 570	gcc Ala	ccc Pro	att Ile	gaa Glu	aaa Lys 575	atc Ile	gct Ala	tct Ser	tct Ser	1784

tat	cgc	tac	ctt	att	tta	ttg	cgt	tcc	aaa	aac	cct	tta	agc	cta	atc	1832
Tyr	Arg	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Lys	Asn	Pro	Leu	Ser	Leu	Ile	
	580					585					590					

aaa agc gtg cat gcg ttt tta aaa tcc gcc cct agt atc cct tgc agc 1880
Lys Ser Val His Ala Phe Leu Lys Ser Ala Pro Ser Ile Pro Cys Ser
595 600 605 610

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615

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Thr	Tyr	Phe	Ser 20	Lys	Glu	Gln	His	Gln 25	Lys	Gly	Ala	Leu 30	Val	Asn	Ile
Pro	Leu	Arg 35	Asn	Lys	Thr	Leu 40	Leu	Gly	Val	Val	Leu 45	Glu	Val	Ser	
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Ala	Asn	Leu	Ser 85	Ser	Val	Leu	Ser	Leu 90	Phe	Ala	Pro	Phe	Lys 95	Glu	Cys
Asp	Leu	Val 100	Gly	Leu	Glu	Lys	Ile	Glu 105	Pro	Ile	Leu	Asn	Ile 110	Leu	Ser
Gln	Thr 115	Gln	Thr	Asn	Ala	Leu	Lys 120	Glu	Leu	Gln	Lys 125	His	Ser	Ala	Ser
Leu 130	Leu	Phe	Gly	Asp 135	Thr	Gly	Ser	Gly	Lys	Thr 140	Glu	Ile	Tyr	Met	His
Ala 145	Ile	Ala	Gln	Thr 150	Leu	Glu	Gln	Lys	Lys 155	Ser	Ala	Leu	Leu	Leu 160	Val
Pro	Glu	Ile	Ala 165	Thr	Pro	Gln	Met	Gln 170	Gln	Arg	Leu	Lys 175	Arg	Val	
Phe	Lys	Glu	Asn 180	Leu	Gly	Leu	Trp	His 185	Ser	Lys	Leu	Ser 190	Gln	Asn	Gln
Lys	Lys 195	Gln	Phe	Leu	Glu	Lys 200	Leu	Tyr	Ser	Gln	Glu	Ile 205	Lys	Leu	Val
Val	Gly 210	Thr	Arg	Ser	Ala	Leu 215	Phe	Leu	Pro	Leu	Lys 220	Glu	Leu	Gly	Leu
Ile 225	Ile	Val	Asp 230	Glu	Glu	His	Asp	Phe	Ser 235	Tyr	Lys	Ser	His	Gln	Ser
Pro	Met	Tyr	Asn 245	Ala	Arg	Asp	Leu	Cys 250	Leu	Tyr	Leu	Ser 255	His	Lys	Phe
Pro	Ile	Gln	Val 260	Ile	Leu	Gly	Ser	Ala 265	Thr	Pro	Ser	Leu 270	Asn	Ser	Tyr
Lys	Arg 275	Phe	Lys	Asp	Lys	Ala 280	Leu	Val	Arg	Leu	Lys 285	Gly	Arg	Tyr	Thr
Pro	Thr 290	Gln	Lys	Asn	Ile 295	Ile	Phe	Glu	Lys	Thr 300	Glu	Arg	Phe	Ile	Thr
Pro	Lys	Leu	Leu	Glu	Ala	Leu	Gln	Gln	Val	Leu	Asp	Lys	Asn	Glu	Gln

305 310 315 320
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325 330 335
Gln Ser Cys Tyr Lys Ser Val Gln Cys Pro Phe Cys Ser Val Asn Met
340 345 350
Ser Leu His Leu Lys Thr Asn Lys Leu Met Cys His Tyr Cys His Phe
355 360 365
Ser Ser Pro Ile Pro Lys Ile Cys Ser Ala Cys Gln Ser Glu Val Leu
370 375 380
Val Gly Lys Arg Ile Gly Thr Met Gln Val Leu Lys Glu Leu Glu Ser
385 390 395 400
Leu Leu Glu Gly Ala Lys Ile Ala Ile Leu Asp Lys Asp His Thr Ser
405 410 415
Thr Gln Lys Lys Leu His Asn Ile Leu Asn Asp Phe Asn Ala Gln Lys
420 425 430
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435 440 445
Ala Lys Val Ser Leu Ala Val Val Leu Gly Ile Asp Asn Ile Ile Lys
450 455 460
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465 470 475 480
Ile Ala Gly Arg Ser Ala Arg Gln Ile Ser Gly Gln Val Phe Ile Gln
485 490 495
Ser Thr Glu Thr Asp Leu Leu Glu Asn Phe Leu Glu Asp Tyr Glu Asp
500 505 510
Phe Leu Gln Tyr Glu Leu Gln Glu Arg Cys Glu Leu Tyr Pro Pro Phe
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Ser Arg Leu Cys Leu Leu Glu Phe Lys His Lys Asn Glu Glu Lys Ala
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Gln Gln Leu Ser Leu Lys Ala Ser Gln Thr Leu Ser Ser Cys Leu Glu
545 550 555 560
Lys Gly Val Thr Leu Ser Asn Phe Lys Ala Pro Ile Glu Lys Ile Ala
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Ser Ser Tyr Arg Tyr Leu Ile Leu Leu Arg Ser Lys Asn Pro Leu Ser
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Met Lys Leu Ser Ile Asn Asp Leu Asn Val
1 5 10
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Phe Val Asn Thr Pro Lys Asp Ile Ala Lys Leu Cys Glu Asp Leu Ser
15 20 25

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aat gtg gtt gtg ggt aaa att tta gaa aaa gcc ccc cat aaa aac gct Asn Val Val Val Gly Lys Ile Leu Glu Lys Ala Pro His Lys Asn Ala 45 50 55	255
gaa aaa ctc agc gtg tgt caa gtg gat gtg ggt aaa gaa gtg ttg caa Glu Lys Leu Ser Val Cys Gln Val Asp Val Gly Lys Glu Val Leu Gln 60 65 70	303
atc gtg tgt ggg gct aaa aat gtc gcg cca aac caa ttc gtg cca gtc Ile Val Cys Gly Ala Lys Asn Val Ala Pro Asn Gln Phe Val Pro Val 75 80 85 90	351
gct tta aac ggg gcg cta atc ggc tca acc acc atc gct aaa acg gag Ala Leu Asn Gly Ala Leu Ile Gly Ser Thr Thr Ile Ala Lys Thr Glu 95 100 105	399
ctt agg ggg gtt gaa agc cat ggc atg att tgc tct agc att gaa tta Leu Arg Gly Val Glu Ser His Gly Met Ile Cys Ser Ser Ile Glu Leu 110 115 120	447
ggc ttc cct aaa atc aat gat ggc atc ttg gaa tta gat gag agc gtt Gly Phe Pro Lys Ile Asn Asp Gly Ile Leu Glu Leu Asp Glu Ser Val 125 130 135	495
ggg gag ttg gtt tta ggg aaa gaa tta aac gaa tac gcc cct ttc aac Gly Glu Leu Val Leu Gly Lys Glu Leu Asn Glu Tyr Ala Pro Phe Asn 140 145 150	543
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agc gtt tta ggt att gcc aga gaa att agc gcc ttt tat cac acg ccc Ser Val Leu Gly Ile Ala Arg Glu Ile Ser Ala Phe Tyr His Thr Pro 175 180 185	639
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acg ctt agt gcg ggt gaa aat att gaa tcg cat ctg gct tat tat ttg Thr Leu Ser Ala Gly Glu Asn Ile Glu Ser His Leu Ala Tyr Tyr Leu 205 210 215	735
att tgc aac cat tca tta aaa acc cct tta aat atc aaa ctt tcg ctc Ile Cys Asn His Ser Leu Lys Thr Pro Leu Asn Ile Lys Leu Ser Leu 220 225 230	783
gct cat aat aat gcc ttg agt gag aac gat ctg aac aat ttc ata gaa Ala His Asn Asn Ala Leu Ser Glu Asn Asp Leu Asn Asn Phe Ile Glu 235 240 245 250	831
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aca acc cct atg gat ttg agc gtg aaa aac gat gaa aac aac ctt gaa Thr Thr Pro Met Asp Leu Ser Val Lys Asn Asp Glu Asn Asn Leu Glu 270 275 280	927
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gcc acg att tta gaa agc aaa caa act gag cat tct tta aaa gat cgc Ala Thr Ile Leu Glu Ser Lys Gln Thr Glu His Ser Leu Lys Asp Arg 365 370 375	1215
acc ctt aca ttc cag ctt gaa gac att act gaa att ttg ggg ctt gct Thr Leu Thr Phe Gln Leu Glu Asp Ile Thr Glu Ile Leu Gly Leu Ala 380 385 390	1263
gta gag aaa gaa aaa att caa ggc att tta aaa aat tta ggc ttt aaa Val Glu Lys Glu Lys Ile Gln Gly Ile Leu Lys Asn Leu Gly Phe Lys 395 400 405 410	1311
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gaa att ttg cgc ttt gta ggg att gat aat cta gtc tca aag ccc ctt Glu Ile Leu Arg Phe Val Gly Ile Asp Asn Leu Val Ser Lys Pro Leu 445 450 455	1455
cat tgt gtc agt agc aaa aat tca aac ccc aat tac gac acg cac cgc His Cys Val Ser Ser Lys Asn Ser Asn Pro Asn Tyr Asp Thr His Arg 460 465 470	1503
ttt ttt gaa aac ctt aaa cac aag gct ctc gct tgc ggt ttt aaa gaa Phe Phe Glu Asn Leu Lys His Lys Ala Leu Ala Cys Gly Phe Lys Glu 475 480 485 490	1551
gtc att cat tac gtg ttt tac tct aaa gaa aaa cag caa aaa tta ggc Val Ile His Tyr Val Phe Tyr Ser Lys Glu Lys Gln Gln Lys Leu Gly	1599

495	500	505	
ttt gaa gtt tta gaa gat ccc cta gaa ttg caa aac cct atc aca acg Phe Glu Val Leu Glu Asp Pro Leu Glu Leu Gln Asn Pro Ile Thr Thr 510 515 520			1647
gag tta aac acc cta agg acg agt ctt gtt tgc ggg ctt tta gac gcc Glu Leu Asn Thr Leu Arg Thr Ser Leu Val Cys Gly Leu Leu Asp Ala 525 530 535			1695
agt tta agg aat aaa aat tta ggg ttt aaa agc ata gcc ctt tat gaa Ser Leu Arg Asn Lys Asn Leu Gly Phe Lys Ser Ile Ala Leu Tyr Glu 540 545 550			1743
aag ggg agc gtg tat aac tct aaa aga gaa gaa atc caa aaa cta ggc Lys Gly Ser Val Tyr Asn Ser Lys Arg Glu Glu Ile Gln Lys Leu Gly 555 560 565 570			1791
ttt tta ata agc ggc ttg caa aaa aaa gaa agc tac cct gat act aag Phe Leu Ile Ser Gly Leu Gln Lys Lys Glu Ser Tyr Pro Asp Thr Lys 575 580 585			1839
ggc aag gct tgg gat ttt tac tct ttt gcc gaa tgc gtt tca aaa gtt Gly Lys Ala Trp Asp Phe Tyr Ser Phe Ala Glu Cys Val Ser Lys Val 590 595 600			1887
ata ggg gat ttc agc ttg gaa aaa cta acc act caa acc ccc att aac Ile Gly Asp Phe Ser Leu Glu Lys Leu Thr Thr Gln Thr Pro Ile Asn 605 610 615			1935
cac ccc tac cag agc gct aaa atc att caa aat cat gaa atc ata ggc His Pro Tyr Gln Ser Ala Lys Ile Ile Gln Asn His Glu Ile Ile Gly 620 625 630			1983
gtg atc gct aaa atc cac cct aaa gtg atc cag gaa ttg gat ttg ttt Val Ile Ala Lys Ile His Pro Lys Val Ile Gln Glu Leu Asp Leu Phe 635 640 645 650			2031
gaa agc tat tac gct gag ata gac gct ttt aaa ctc aaa cgc cct gct Glu Ser Tyr Tyr Ala Glu Ile Asp Ala Phe Lys Leu Lys Arg Pro Ala 655 660 665			2079
atg cta tta aaa ccc ttt agc att tat cct agc agt gtt agg gat ttg Met Leu Leu Lys Pro Phe Ser Ile Tyr Pro Ser Ser Val Arg Asp Leu 670 675 680			2127
act ctc atc att gat gag aat acc gct ttt agt ggg att aaa aaa gcc Thr Leu Ile Ile Asp Glu Asn Thr Ala Phe Ser Gly Ile Lys Lys Ala 685 690 695			2175
cta aag gac gct caa atc cct aat tta agc gag att cta ccc ctt gat Leu Lys Asp Ala Gln Ile Pro Asn Leu Ser Glu Ile Leu Pro Leu Asp 700 705 710			2223
att ttt aaa gaa agt aat aat tcc ata gcc tta agc gtg cgt tgc gtg Ile Phe Lys Glu Ser Asn Asn Ser Ile Ala Leu Ser Val Arg Cys Val 715 720 725 730			2271
atc cat tct tta gaa aaa acc ctg aat gat gaa gag gtc aat tca gcc			2319

Ser	Leu	Lys	Leu	His	Ala	Leu	Lys	Asp	Lys	Thr	Leu	Gln	Lys	Asp	Asn
				325					330					335	
Ala	Leu	Ile	Tyr	Arg	Ser	Ala	Arg	Gly	Ser	Asn	Pro	Asn	Leu	Ser	Asp
			340					345					350		
Gly	Leu	Asn	Phe	Leu	Ser	Ala	His	Leu	Lys	Ala	Thr	Ile	Leu	Glu	Ser
		355					360					365			
Lys	Gln	Thr	Glu	His	Ser	Leu	Lys	Asp	Arg	Thr	Leu	Thr	Phe	Gln	Leu
	370					375					380				
Glu	Asp	Ile	Thr	Glu	Ile	Leu	Gly	Leu	Ala	Val	Glu	Lys	Glu	Lys	Ile
385					390					395					400
Gln	Gly	Ile	Leu	Lys	Asn	Leu	Gly	Phe	Lys	Val	Ser	Val	Lys	Glu	Pro
				405					410					415	
Asn	Ser	Lys	Pro	Gln	Ile	Leu	Glu	Val	Ile	Ala	Pro	Asn	Phe	Arg	His
			420					425					430		
Asp	Ile	Lys	Thr	Ile	Gln	Asp	Ile	Ala	Glu	Glu	Ile	Leu	Arg	Phe	Val
		435					440					445			
Gly	Ile	Asp	Asn	Leu	Val	Ser	Lys	Pro	Leu	His	Cys	Val	Ser	Ser	Lys
	450					455					460				
Asn	Ser	Asn	Pro	Asn	Tyr	Asp	Thr	His	Arg	Phe	Phe	Glu	Asn	Leu	Lys
465					470					475					480
His	Lys	Ala	Leu	Ala	Cys	Gly	Phe	Lys	Glu	Val	Ile	His	Tyr	Val	Phe
				485					490					495	
Tyr	Ser	Lys	Glu	Lys	Gln	Gln	Lys	Leu	Gly	Phe	Glu	Val	Leu	Glu	Asp
			500					505					510		
Pro	Leu	Glu	Leu	Gln	Asn	Pro	Ile	Thr	Thr	Glu	Leu	Asn	Thr	Leu	Arg
		515					520					525			
Thr	Ser	Leu	Val	Cys	Gly	Leu	Leu	Asp	Ala	Ser	Leu	Arg	Asn	Lys	Asn
	530				535						540				
Leu	Gly	Phe	Lys	Ser	Ile	Ala	Leu	Tyr	Glu	Lys	Gly	Ser	Val	Tyr	Asn
545					550					555					560
Ser	Lys	Arg	Glu	Glu	Ile	Gln	Lys	Leu	Gly	Phe	Leu	Ile	Ser	Gly	Leu
				565					570					575	
Gln	Lys	Lys	Glu	Ser	Tyr	Pro	Asp	Thr	Lys	Gly	Lys	Ala	Trp	Asp	Phe
			580					585					590		
Tyr	Ser	Phe	Ala	Glu	Cys	Val	Ser	Lys	Val	Ile	Gly	Asp	Phe	Ser	Leu
		595					600					605			
Glu	Lys	Leu	Thr	Thr	Gln	Thr	Pro	Ile	Asn	His	Pro	Tyr	Gln	Ser	Ala
	610					615					620				
Lys	Ile	Ile	Gln	Asn	His	Glu	Ile	Ile	Gly	Val	Ile	Ala	Lys	Ile	His
625				630						635					640
Pro	Lys	Val	Ile	Gln	Glu	Leu	Asp	Leu	Phe	Glu	Ser	Tyr	Tyr	Ala	Glu
				645					650					655	
Ile	Asp	Ala	Phe	Lys	Leu	Lys	Arg	Pro	Ala	Met	Leu	Leu	Lys	Pro	Phe
			660					665					670		
Ser	Ile	Tyr</													

-382-

[illegible]

<400> 329

-383-

gaa act gat ttg aga gtg ttg gag agc ttt taatgaaact gagcattaat 1060
 Glu Thr Asp Leu Arg Val Leu Glu Ser Phe
 175 180

gatttgaatg tttttgtcaa tacgcctaaa gatatag 1097

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 <211> 183
 <212> PRT
 <213> Helicobacter pylori

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 Thr Ser Pro Val Gln Ile His Thr Met Gln Glu Gln Thr Pro Pro Ile
 20 25 30
 Lys Met Ile Cys Leu Gly Glu Thr Phe Arg Arg Asp Tyr Asp Leu Thr
 35 40 45
 His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val Asp Gln Lys
 50 55 60
 Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu Asp Phe Leu
 65 70 75 80
 His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser Ser Phe Phe
 85 90 95
 Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys Val Phe Cys
 100 105 110
 Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp Leu Glu Val
 115 120 125
 Leu Gly Cys Gly Met Val Asn Asn Ala Val Phe Glu Ala Ile Gly Tyr
 130 135 140
 Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu Arg Leu Ala
 145 150 155 160
 Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe Glu Thr Asp
 165 170 175
 Leu Arg Val Leu Glu Ser Phe
 180

<210> 331
 <211> 517
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(464)

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 Met Lys
 1

aaa att gat gat atg aga cac gga aga cat tgt gtt ttt tta atg cat 104
 Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His
 5 10 15

gtg cat ttt gta ttt gtt act aaa tac agg cgt tca gca ttc aat aag 152
 Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe Asn Lys
 20 25 30

gaa gtg ata gat ttt tta gga tcg gtg ttt gcc aaa gtg tgt aag gac	200
Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys Lys Asp	
35 40 45 50	
ttt gag agc gaa ttg gta gaa ttt gat ggg gag agc gat cat gtg cat	248
Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His Val His	
55 60 65	
ttg ctt atc aac tac cct cca aaa gtg agc gtg agt aag tta gtt aat	296
Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu Val Asn	
70 75 80	
tct tta aaa ggc gtt agc agt cgt ttg act aga caa cac cat ttc aaa	344
Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His Phe Lys	
85 90 95	
agc gtt gaa gct agt ttg tgg ggg aag cat tta tgg tcg cct agt tat	392
Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro Ser Tyr	
100 105 110	
ttc gct ggg agt tgt ggg gac gcg cct tta gag atg att aag caa tac	440
Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys Gln Tyr	
115 120 125 130	
ata caa gat caa gaa aca ccg cat taaattagct aacttttgatt tttaagtaga	494
Ile Gln Asp Gln Glu Thr Pro His	
135	
acgcgcctaaa aagcgaatgg atc	517
<210> 332	
<211> 138	
<212> PRT	
<213> Helicobacter pylori	
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Met Lys Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu	
1 5 10 15	
Met His Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe	
20 25 30	
Asn Lys Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys	
35 40 45	
Lys Asp Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His	
50 55 60	
Val His Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu	
65 70 75 80	
Val Asn Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His	
85 90 95	
Phe Lys Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro	
100 105 110	
Ser Tyr Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys	
115 120 125	
Gln Tyr Ile Gln Asp Gln Glu Thr Pro His	
130 135	
<210> 333	
<211> 1786	
<212> DNA	

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1733)

<400> 333

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1	
gaa gtc cat gat tat ggg att aaa ttt tgg agc aat aac gaa ttt aag	104
Glu Val His Asp Tyr Gly Ile Lys Phe Trp Ser Asn Asn Glu Phe Lys	
5 10 15	
ata gaa aaa ggc ttg gtt aaa gtc tgt cat ggt aaa aac ccc tcg ctt	152
Ile Glu Lys Gly Leu Val Lys Val Cys His Gly Lys Asn Pro Ser Leu	
20 25 30	
tta gaa atc gtt caa agc gtg cgc gat aag ggc tat aga gga cct ttg	200
Leu Glu Ile Val Gln Ser Val Arg Asp Lys Gly Tyr Arg Gly Pro Leu	
35 40 45 50	
ttg gtg cga ttc ccc cat ttg gtg caa aaa caa atc aaa agc ctg ttt	248
Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser Leu Phe	
55 60 65	
gat gcg ttt tct tca gcg att aaa gag tat caa tac agc ggg gct ttt	296
Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly Ala Phe	
70 75 80	
aag gcg gtt ttc cct tta aaa gtc aat caa atg ccc tcg ttt gtt ttc	344
Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe Val Phe	
85 90 95	
cct tta gtg cag ggg gct aag ggt ttg aat tac gga tta gag gct ggg	392
Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu Ala Gly	
100 105 110	
agc aag tct gaa ctc atc atc gca atg agt tac act aac cct aaa gcc	440
Ser Lys Ser Glu Leu Ile Ile Ala Met Ser Tyr Thr Asn Pro Lys Ala	
115 120 125 130	
cct atc acc gtg aat ggc ttt aaa gac aaa gaa atg att gag ctt ggc	488
Pro Ile Thr Val Asn Gly Phe Lys Asp Lys Glu Met Ile Glu Leu Gly	
135 140 145	
ttt atc gct aaa agc atg cag cat gag atc act tta acg att gag ggt	536
Phe Ile Ala Lys Ser Met Gln His Glu Ile Thr Leu Thr Ile Glu Gly	
150 155 160	
ttg aat gaa ttg aaa acc att atc gcc gtg gct aaa caa aac gag ttt	584
Leu Asn Glu Leu Lys Thr Ile Ile Ala Val Ala Lys Gln Asn Glu Phe	
165 170 175	
tta gcc tgc cct aaa att ggc atc cgc atc cgt ttg cac agc act ggc	632
Leu Ala Cys Pro Lys Ile Gly Ile Arg Ile Arg Leu His Ser Thr Gly	
180 185 190	

act Thr 195	ggc Gly	gtt Val	tgg Trp	gca Ala	aag Lys 200	agt Ser	ggg Gly	ggg Gly	atc Ile	aat Asn 205	tct Ser	aaa Lys	ttt Phe	ggg Gly	ctt Leu 210	680
agc Ser	agc Ser	act Thr	gaa Glu	gtt Val 215	tta Leu	gag Glu	gcg Ala	atg Met	cgc Arg 220	ctt Leu	tta Leu	gaa Glu	gaa Glu	aac Asn 225	gac Asp	728
ttg Leu	tta Leu	gag Glu	cat His 230	ttc Phe	cac His	atg Met	ata Ile	cat His 235	ttc Phe	cat His	ata Ile	ggc Gly	tct Ser 240	caa Gln	atc Ile	776
agc Ser	gat Asp	att Ile 245	tcg Ser	ccc Pro	tta Leu	aaa Lys	aag Lys 250	gct Ala	tta Leu	aga Arg	gaa Glu	gcg Ala 255	ggg Gly	aac Asn	ttg Leu	824
tat Tyr 260	gca Ala	gaa Glu	ttg Leu	cgt Arg	aaa Lys 265	atg Met	ggc Gly	gct Ala	aaa Lys	aat Asn 270	ctt Leu	aat Asn	agc Ser	gtg Val	aat Asn	872
att Ile 275	gga Gly	ggg Gly	ggg Gly	tta Leu 280	gcc Ala	gta Val	gaa Glu	tac Tyr	acc Thr 285	caa Gln	cac His	aag Lys	cac His	cac His	caa Gln 290	920
gac Asp	aaa Lys	aac Asn	tac Tyr 295	act Thr	tta Leu	gag Glu	gaa Glu	ttc Phe	agc Ser 300	gct Ala	gat Asp	gtg Val	gtg Val	ttt Phe 305	tta Leu	968
ttg Leu	aga Arg	gaa Glu	att Ile 310	gtg Val	aaa Lys	aat Asn	aag Lys	cag Gln 315	gaa Glu	atc Ile	gag Glu	ccg Pro 320	gac Asp	att Ile	ttc Phe	1016
att Ile	gaa Glu	tca Ser 325	ggc Gly	cgt Arg	tat Tyr	att Ile	tcc Ser 330	gct Ala	aac Asn	cat His	gcc Ala	gtt Val 335	tta Leu	gtg Val	gcc Ala	1064
ccg Pro 340	gtg Val	tta Leu	gaa Glu	ttg Leu	ttt Phe	tcg Ser 345	cat His	gaa Glu	tac Tyr	aat Asn 350	gaa Glu	aaa Lys	tcc Ser	cta Leu	aaa Lys	1112
atc Ile 355	aaa Lys	gaa Glu	aat Asn	aat Asn 360	aac Asn	ccc Pro	cct Pro	ttg Leu	att Ile 365	gat Asp	gaa Glu	atg Met	cta Leu	gac Asp	ttg Leu 370	1160
ctc Leu	gct Ala	aat Asn	atc Ile	aat Asn 375	gaa Glu	aaa Lys	aac Asn	gcc Ala	att Ile 380	gaa Glu	tac Tyr	ttg Leu	cat His	gat Asp	agt Ser 385	1208
ttt Phe	gat Asp	cac His	acc Thr 390	gag Glu	tcg Ser	cta Leu	ttc Phe	acg Thr 395	ctt Leu	ttt Phe	gat Asp	ctg Leu	ggc Gly 400	tat Tyr	att Ile	1256
gat Asp	ttg Leu	att Ile 405	gac Asp	agg Arg	agc Ser	aac Asn	act Thr 410	gaa Glu	gtt Val	tta Leu	gcc Ala	cat His 415	ttg Leu	atc Ile	gtc Val	1304
aaa Lys 420	aaa Lys	gcg Ala	gtg Val	caa Gln	ttg Leu 425	ctt Leu	tat Tyr	gtt Val	aag Lys	gat Asp 430	cat His	aac Asn	gat Asp	att Ile	tta Leu	1352

[illegible]

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<210> 335
<211> 676
<212> DNA
<213> Helicobacter pylori
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<220>
 <221> CDS
 <222> (51)...(623)

<400> 335

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Met Asp	
1	
gaa gtc tta aaa gag att tta tca agt tat caa aaa aga gct tta aaa	104
Glu Val Leu Lys Glu Ile Leu Ser Ser Tyr Gln Lys Arg Ala Leu Lys	
5 10 15	
tta acc aaa aga gtt aga aag aag att ttt aag aat gat ccc aca gaa	152
Leu Thr Lys Arg Val Arg Lys Lys Ile Phe Lys Asn Asp Pro Thr Glu	
20 25 30	
aat caa aaa aaa gcc ata aag atc gct cta aat acc cct gat att gct	200
Asn Gln Lys Lys Ala Ile Lys Ile Ala Leu Asn Thr Pro Asp Ile Ala	
35 40 45 50	
att atc caa ggg cct cct gga acg ggc aaa acc act gtg atc aat gcc	248
Ile Ile Gln Gly Pro Pro Gly Thr Gly Lys Thr Thr Val Ile Asn Ala	
55 60 65	
att tgt gag aga ttg ttt gaa gaa tac cct aag gat aaa aat atc aag	296
Ile Cys Glu Arg Leu Phe Glu Glu Tyr Pro Lys Asp Lys Asn Ile Lys	
70 75 80	
ggg caa att tta ctg tgc gct caa ggg cat gat gcg act aac aat gcg	344
Gly Gln Ile Leu Leu Cys Ala Gln Gly His Asp Ala Thr Asn Asn Ala	
85 90 95	
cgt gag cgc atc aaa gta ggg gga ttg ccc act ttt aaa ttt ggt gct	392
Arg Glu Arg Ile Lys Val Gly Gly Leu Pro Thr Phe Lys Phe Gly Ala	
100 105 110	
aaa aaa aat gct aaa gaa gaa caa tac aag caa gat gaa aga ttg aat	440
Lys Lys Asn Ala Lys Glu Glu Gln Tyr Lys Gln Asp Glu Arg Leu Asn	
115 120 125 130	
gag cga ttg aga gag ttt gct gaa acg ctc ata gaa agc gtg aga aaa	488
Glu Arg Leu Arg Glu Phe Ala Glu Thr Leu Ile Glu Ser Val Arg Lys	
135 140 145	
aaa ctg caa aaa tta ggg gat tat gaa aat ata gaa aaa att ttg gat	536
Lys Leu Gln Lys Leu Gly Asp Tyr Glu Asn Ile Glu Lys Ile Leu Asp	
150 155 160	
tta gaa gaa gcc ctt aga cgc tac tat agt tcg cct atc agt gaa ttg	584
Leu Glu Glu Ala Leu Arg Arg Tyr Tyr Ser Ser Pro Ile Ser Glu Leu	
165 170 175	
gaa ttt tta aaa gaa ata gaa aaa aat gag agc ttt ttt taattcttct	633
Glu Phe Leu Lys Glu Ile Glu Lys Asn Glu Ser Phe Phe	
180 185 190	
atgcgtgaaa agctaagcca attaaaagca aggcagcaaaa aac	676

<210> 336
 <211> 191
 <212> PRT
 <213> Helicobacter pylori

<400> 336
 Met Asp Glu Val Leu Lys Glu Ile Leu Ser Ser Tyr Gln Lys Arg Ala
 1 5 10 15
 Leu Lys Leu Thr Lys Arg Val Arg Lys Lys Ile Phe Lys Asn Asp Pro
 20 25 30
 Thr Glu Asn Gln Lys Lys Ala Ile Lys Ile Ala Leu Asn Thr Pro Asp
 35 40 45
 Ile Ala Ile Ile Gln Gly Pro Pro Gly Thr Gly Lys Thr Thr Val Ile
 50 55 60
 Asn Ala Ile Cys Glu Arg Leu Phe Glu Glu Tyr Pro Lys Asp Lys Asn
 65 70 75 80
 Ile Lys Gly Gln Ile Leu Leu Cys Ala Gln Gly His Asp Ala Thr Asn
 85 90 95
 Asn Ala Arg Glu Arg Ile Lys Val Gly Gly Leu Pro Thr Phe Lys Phe
 100 105 110
 Gly Ala Lys Lys Asn Ala Lys Glu Glu Gln Tyr Lys Gln Asp Glu Arg
 115 120 125
 Leu Asn Glu Arg Leu Arg Glu Phe Ala Glu Thr Leu Ile Glu Ser Val
 130 135 140
 Arg Lys Lys Leu Gln Lys Leu Gly Asp Tyr Glu Asn Ile Glu Lys Ile
 145 150 155 160
 Leu Asp Leu Glu Glu Ala Leu Arg Arg Tyr Tyr Ser Ser Pro Ile Ser
 165 170 175
 Glu Leu Glu Phe Leu Lys Glu Ile Glu Lys Asn Glu Ser Phe Phe
 180 185 190

<210> 337
 <211> 913
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (86)...(862)

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 Met Gln Glu Arg Val Phe Lys Arg Lys
 1 5
 gtt tta gat gcg aat atc tta aaa gaa atg cat gcg aac aat gtc tgt 160
 Val Leu Asp Ala Asn Ile Leu Lys Glu Met His Ala Asn Asn Val Cys 25
 10 15 20
 tat tcc aag cat tca aaa gat agg ttt att cct ttc aaa ttt gat aaa 208
 Tyr Ser Lys His Ser Lys Asp Arg Phe Ile Pro Phe Lys Phe Asp Lys 30 35 40
 ttt ggt tat gtt gga tgt aaa ctt ttt aaa aag ata tta aac ttt cct 256
 Phe Gly Tyr Val Gly Cys Lys Leu Phe Lys Lys Ile Leu Asn Phe Pro 45 50 55
 agc aat aca act ttc ttt ggt ggc aca ggt tgt aag aaa ctc atg gaa 304

Met Gln Glu Arg Val Phe Lys Arg Lys Val Leu Asp Ala Asn Ile Leu
 1 5 10 15
 Lys Glu Met His Ala Asn Asn Val Cys Tyr Ser Lys His Ser Lys Asp
 20 25 30
 Arg Phe Ile Pro Phe Lys Phe Asp Lys Phe Gly Tyr Val Gly Cys Lys
 35 40 45
 Leu Phe Lys Lys Ile Leu Asn Phe Pro Ser Asn Thr Thr Phe Phe Gly
 50 55 60
 Gly Thr Gly Cys Lys Lys Leu Met Glu Leu Leu Ser Glu Ile Val Ile
 65 70 75 80
 Asp Ser Arg Ser Ser Lys Ile Ala Leu Asn Arg His Tyr Ala Leu Thr
 85 90 95
 Arg Leu Gln Trp Cys Asp Arg Thr Leu Arg His Asn Leu Gln Ile Leu
 100 105 110
 Glu Arg Ile Gly Phe Leu Thr Ala Phe Lys Asn Lys Lys Gly Tyr Ile
 115 120 125
 Phe Leu Ser Met His Asp Phe Thr Lys Ile Glu Asn Tyr Glu His Ser
 130 135 140
 Gly Leu Asn Gly Glu Ser Asn Leu Pro Asn Ser Phe Phe Leu Gly Ile
 145 150 155 160
 Cys Gly Tyr Leu Lys Lys Leu Phe Lys Lys Leu Lys Asp Arg Ala Phe
 165 170 175
 Arg Leu Ala Asn Lys His Gly Val Phe Phe Leu Lys Ile Pro Lys His
 180 185 190
 Phe Gln Met Gln Asn Phe Asn Asn Ile Phe Leu Glu Phe Val Ser Val
 195 200 205
 Asn Asn Pro Cys Phe Ser Tyr Arg Leu Thr Tyr Asp Gln Leu Val Gly
 210 215 220
 Lys Lys Ile Pro Asn Ile Lys Cys Ser Tyr Gln Gln Ala Ile Val Lys
 225 230 235 240
 Lys Asn Ile His Arg Ala Leu Asp Glu Leu Ser Ile Asp Lys Glu Ile
 245 250 255
 Leu Ala Ser

<210> 339
 <211> 3166
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(3113)

<400> 339
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 Met Asp
 1
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 Leu Glu Glu Leu Tyr Ala Pro Asn His Ile Glu Arg Leu Lys Ala Arg
 5 10 15
 agt ttt tta aga tcg att gct ttt ttt gat gat ttt agc gct tct ttt 152
 Ser Phe Leu Arg Ser Ile Ala Phe Phe Asp Asp Phe Ser Ala Ser Phe
 20 25 30
 gaa tac aga gat cta ttt agc gtt ttg gaa aat atc gtg caa ttt gat 200
 Glu Tyr Arg Asp Leu Phe Ser Val Leu Glu Asn Ile Val Gln Phe Asp

35					40					45					50					
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Gln	Ile	Asp	Glu	Lys	Gln	Ala	Ile	Ile	Pro	Asn	Asn	Leu	Leu	His	Phe					
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-401-

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Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys Tyr Pro	
135 140 145	
aat aaa aaa gcg att aaa gcg cat aaa acc act tgt aaa agc cca aaa	536
Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser Pro Lys	
150 155 160	
acc agc act tct tgt ttg atg gat ttg agc ttg tca aaa tta aac tca	584
Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu Asn Ser	
165 170 175	
atg cct atc ata aac att aaa aag acg ata cca aat tcg cca ata tca	632
Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro Ile Ser	
180 185 190	
gac aac aaa tca aaa tca tta att tta aaa aaa gcc gct aag acc gtt	680
Asp Asn Lys Ser Lys Ser Leu Ile Leu Lys Lys Ala Ala Lys Thr Val	
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Pro Val Gln Met	
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35 40 45	
Pro Phe Phe Pro Gly Asn Asn Lys Arg Thr Lys Ile Ile Pro Ala Glu	
50 55 60	
Ile Lys Val Leu Arg Met Ser Lys Leu Thr Leu Glu Ser Leu Leu Pro	
65 70 75 80	
Arg Ile Val Arg Ile Lys Ser Met Gly Met Ala Ala Ile Ser Trp Lys	
85 90 95	
Ile Lys Ile Pro Thr Ala Leu Phe Pro Met Gly Val Leu Ser Cys Leu	
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Glu Ser Ser Lys Asn Phe Ser Thr Ile Ala Val Glu Glu Ser Glu Ser	
115 120 125	
Pro Met Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys	
130 135 140	
Tyr Pro Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser	
145 150 155 160	
Pro Lys Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu	
165 170 175	
Asn Ser Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro	
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195 200 205	

Thr Val Pro Val Gln Met
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<212> DNA
<213> Helicobacter pylori

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<400> 345
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Met Arg
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Leu Glu Asn Leu Ser Gln Gln Lys Ile Leu Gln Leu Ser Gly Gly Gln
5 10 15

gcc caa cga gtc gct tta gca aga gct tta atc gca gcc aag aat cta 152
Ala Gln Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu
20 25 30

ttg ctt tta gat gag cct tta aac gcc tta gat aac gcc tta aaa aac 200
Leu Leu Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn
35 40 45 50

gaa gtg caa caa ggt ttg ctt gat ttt atc aag cgt gaa aat tta agc 248
Glu Val Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser
55 60 65

gtg tta ttg gta agc cat aac ccc aat gaa atc acc aag ctc gcg caa 296
Val Leu Leu Val Ser His Asn Pro Asn Glu Ile Thr Lys Leu Ala Gln
70 75 80

act ttc ctc ttt tta aac aat ggc gtt att gat cct aat caa gaa aat 344
Thr Phe Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn
85 90 95

cgg ctt ttt tca aac cgc tta tta ata aaa cct ctc ttt gaa gat gaa 392
Arg Leu Phe Ser Asn Arg Leu Leu Ile Lys Pro Leu Phe Glu Asp Glu
100 105 110

aat tat tgc cat tat gag gtc att tct caa acg att agt ttg ccc aaa 440
Asn Tyr Cys His Tyr Glu Val Ile Ser Gln Thr Ile Ser Leu Pro Lys
115 120 125 130

gat tgt ctg aac cca act ttt aag ctt gat ttc aat caa aac aaa aaa 488
Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp Phe Asn Gln Asn Lys Lys
135 140 145

ttt tagaaatatt ttttcatttt cctcttaaaa ccctcttatt tttcaaaagg 541
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<210> 346
<211> 147
<212> PRT

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<211> 1530

<212> DNA

<213> Helicobacter pylori

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<400> 347

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ttg	atc	gtt	acg	cgc	ttc	gct	cca	tcg	ccc	act	ggc	tac	ctc	cac	ata		105
Leu	Ile	Val	Thr	Arg	Phe	Ala	Pro	Ser	Pro	Thr	Gly	Tyr	Leu	His	Ile		
		5					10					15					
gga	ggc	tta	aga	aca	gcc	att	ttc	aat	tat	ctt	ttt	gca	cga	gcc	aat		153
Gly	Gly	Leu	Arg	Thr	Ala	Ile	Phe	Asn	Tyr	Leu	Phe	Ala	Arg	Ala	Asn		
	20					25					30						
caa	gga	aaa	ttt	ttt	tta	cgc	att	gaa	gac	acg	gat	ttg	agc	cgt	aac		201
Gln	Gly	Lys	Phe	Phe	Leu	Arg	Ile	Glu	Asp	Thr	Asp	Leu	Ser	Arg	Asn		
	35				40					45					50		
tct	ata	gaa	gcg	gct	aac	gcc	att	ata	gaa	gct	ttc	aaa	tgg	gta	ggg		249
Ser	Ile	Glu	Ala	Ala	Asn	Ala	Ile	Ile	Glu	Ala	Phe	Lys	Trp	Val	Gly		
				55					60					65			
cta	gaa	tac	gat	ggc	gaa	atc	ctc	tac	caa	tcc	aaa	cgc	ttt	gag	att		297
Leu	Glu	Tyr	Asp	Gly	Glu	Ile	Leu	Tyr	Gln	Ser	Lys	Arg	Phe	Glu	Ile		
			70					75					80				
tat	aaa	gaa	tac	att	caa	aaa	ctc	tta	gat	gaa	gac	aaa	gcc	tat	tat		345

Tyr	Lys	Glu	Tyr	Ile	Gln	Lys	Leu	Leu	Asp	Glu	Asp	Lys	Ala	Tyr	Tyr		
		85					90					95					
tgt	tac	atg	agc	aaa	gaa	gag	ttg	gac	gct	ttg	aga	gaa	gag	caa	aaa	393	
Cys	Tyr	Met	Ser	Lys	Glu	Glu	Leu	Asp	Ala	Leu	Arg	Glu	Glu	Gln	Lys		
	100					105					110						
gcc	agg	aaa	gaa	acc	cca	cgc	tat	gac	aat	cgc	tat	cgt	gat	ttt	aaa	441	
Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp	Phe	Lys		
115					120					125					130		
ggc	acg	cct	cct	aaa	ggc	ata	gag	cct	gtg	gta	agg	att	aaa	gtc	ccc	489	
Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys	Val	Pro		
				135					140					145			
caa	aat	gag	gtg	att	ggc	ttt	aat	gac	ggg	gtt	aaa	ggc	gaa	gtg	aaa	537	
Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu	Val	Lys		
			150					155					160				
gtg	aat	act	aac	gaa	tta	gac	gat	ttt	att	atc	gcc	agg	agc	gat	ggg	585	
Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser	Asp	Gly		
		165					170					175					
aca	ccc	act	tat	aac	ttt	gtg	gtt	act	att	gat	gac	gct	tta	atg	ggg	633	
Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu	Met	Gly		
	180					185					190						
att	act	gat	gtg	att	aga	ggc	gat	gat	cac	ctt	tct	aac	acc	cct	aaa	681	
Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr	Pro	Lys		
195					200					205					210		
caa	atc	gtt	ctt	tat	aag	gct	ttg	aat	ttt	aaa	atc	cct	aat	ttt	ttc	729	
Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn	Phe	Phe		
				215					220					225			
cat	gtg	ccg	atg	att	ttg	aat	gaa	gaa	ggg	caa	aaa	tta	agc	aaa	cgc	777	
His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser	Lys	Arg		
			230					235					240				
cat	ggg	gcc	act	aat	gtg	atg	gac	tat	caa	gaa	atg	ggc	tat	ctt	aag	825	
His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr	Leu	Lys		
		245					250					255					
gaa	gct	tta	gtg	aat	ttt	tta	gcg	cgt	ttg	ggg	tgg	agc	tat	cag	gat	873	
Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr	Gln	Asp		
	260					265					270						
aaa	gag	gtt	ttt	agc	atg	caa	gaa	ttg	cta	gaa	tta	ttt	gat	cct	aaa	921	
Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp	Pro	Lys		
275					280					285					290		
gat	ttg	aat	tct	tcg	ccc	agt	tgc	ttc	agc	tgg	cac	aag	ctt	aat	tgg	969	
Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu	Asn	Trp		
				295					300					305			
ctc	aac	gct	cat	tat	tta	aaa	aac	caa	agt	gtg	caa	gaa	ttg	tta	aaa	1017	
Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu	Leu	Lys		
			310					315					320				

ctt tta aag cct ttt agt ttt agc gat ctc tgc cat tta aac ccc act	1065
Leu Leu Lys Pro Phe Ser Phe Ser Asp Leu Ser His Leu Asn Pro Thr	
325 330 335	
caa ttg gat cgc ttg tta gac gct ctc aaa gaa aga tct caa aca cta	1113
Gln Leu Asp Arg Leu Leu Asp Ala Leu Lys Glu Arg Ser Gln Thr Leu	
340 345 350	
aaa gaa tta gcc ctt aaa ata gat gag gtt tta atc gcc cct gtg gag	1161
Lys Glu Leu Ala Leu Lys Ile Asp Glu Val Leu Ile Ala Pro Val Glu	
355 360 365 370	
tat gaa gaa aag gtt ttt aaa aaa ctc aat caa gcg ctc gtt atg ccc	1209
Tyr Glu Glu Lys Val Phe Lys Lys Leu Asn Gln Ala Leu Val Met Pro	
375 380 385	
ttg tta gaa aag ttt aag cta gaa tta aac aaa gcc aat ttc aac gat	1257
Leu Leu Glu Lys Phe Lys Leu Glu Leu Asn Lys Ala Asn Phe Asn Asp	
390 395 400	
gaa agc gcg cta gaa aac gcc atg cgc caa atc att gaa gaa gaa aag	1305
Glu Ser Ala Leu Glu Asn Ala Met Arg Gln Ile Ile Glu Glu Glu Lys	
405 410 415	
att aaa gcg ggt agt ttt atg cag cct tta aga ttg gcc ctt ttg ggt	1353
Ile Lys Ala Gly Ser Phe Met Gln Pro Leu Arg Leu Ala Leu Leu Gly	
420 425 430	
aag gga ggc ggg ata ggc ctt aaa gaa gcg ctt ttt att tta ggc aaa	1401
Lys Gly Gly Gly Ile Gly Leu Lys Glu Ala Leu Phe Ile Leu Gly Lys	
435 440 445 450	
aca gag agc gtc aaa aga ata gag gat ttt ttg aaa aac taaaaaattg	1450
Thr Glu Ser Val Lys Arg Ile Glu Asp Phe Leu Lys Asn	
455 460	
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<211> 463

<212> PRT

<213> Helicobacter pylori

<400> 348

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Ala Asn Gln Gly Lys Phe Phe Leu Arg Ile Glu Asp Thr Asp Leu Ser	
35 40 45	
Arg Asn Ser Ile Glu Ala Ala Asn Ala Ile Ile Glu Ala Phe Lys Trp	
50 55 60	
Val Gly Leu Glu Tyr Asp Gly Glu Ile Leu Tyr Gln Ser Lys Arg Phe	
65 70 75 80	
Glu Ile Tyr Lys Glu Tyr Ile Gln Lys Leu Leu Asp Glu Asp Lys Ala	
85 90 95	
Tyr Tyr Cys Tyr Met Ser Lys Glu Glu Leu Asp Ala Leu Arg Glu Glu	
100 105 110	

Gln	Lys	Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp
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Phe	Lys	Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys
	130					135					140				
Val	Pro	Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu
	145			150						155					160
Val	Lys	Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser
			165					170						175	
Asp	Gly	Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu
		180					185						190		
Met	Gly	Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr
	195						200					205			
Pro	Lys	Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn
	210					215					220				
Phe	Phe	His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser
	225				230					235					240
Lys	Arg	His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr
			245					250						255	
Leu	Lys	Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr
		260					265						270		
Gln	Asp	Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp
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Pro	Lys	Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu
	290					295					300				
Asn	Trp	Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu
	305				310					315					320
Leu	Lys	Leu	Leu	Lys	Pro	Phe	Ser	Phe	Ser	Asp	Leu	Ser	His	Leu	Asn
			325					330						335	
Pro	Thr	Gln	Leu	Asp	Arg	Leu	Leu	Asp	Ala	Leu	Lys	Glu	Arg	Ser	Gln
			340					345					350		
Thr	Leu	Lys	Glu	Leu	Ala	Leu	Lys	Ile	Asp	Glu	Val	Leu	Ile	Ala	Pro
	355					360						365			
Val	Glu	Tyr	Glu	Glu	Lys	Val	Phe	Lys	Lys	Leu	Asn	Gln	Ala	Leu	Val
	370					375					380				
Met	Pro	Leu	Leu	Glu	Lys	Phe	Lys	Leu	Glu	Leu	Asn	Lys	Ala	Asn	Phe
	385				390					395					400
Asn	Asp	Glu	Ser	Ala	Leu	Glu	Asn	Ala	Met	Arg	Gln	Ile	Ile	Glu	Glu
			405						410					415	
Glu	Lys	Ile	Lys	Ala	Gly	Ser	Phe	Met	Gln	Pro	Leu	Arg	Leu	Ala	Leu
			420				425						430		
Leu	Gly	Lys	Gly	Gly	Gly	Ile	Gly	Leu	Lys	Glu	Ala	Leu	Phe	Ile	Leu
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 <213> Helicobacter pylori

<220>
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 Met Phe
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gca gac gca acc aca cta tta gga ttt ttt gaa gaa aat caa aac aat      275
Ala Asp Ala Thr Thr Leu Leu Gly Phe Phe Glu Glu Asn Gln Asn Asn
          20          25          30
caa ttt gtc att cct atc tat cag agg ttg tat agt tgg aaa aag gaa      323
Gln Phe Val Ile Pro Ile Tyr Gln Arg Leu Tyr Ser Trp Lys Lys Glu
          35          40          45
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<212> PRT
<213> Helicobacter pylori

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          20          25          30
Phe Val Ile Pro Ile Tyr Gln Arg Leu Tyr Ser Trp Lys Lys Glu
          35          40          45

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<212> DNA
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<220>
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                               Met Arg
                               1
ctt tat caa aaa caa ggc ttg gaa atg gtg ggt caa aag ttg gat tct      104
Leu Tyr Gln Lys Gln Gly Leu Glu Met Val Gly Gln Lys Leu Asp Ser
          5          10          15
tat tta gcg gat aaa tct ttt tgg gca gaa gaa ctt caa aac aag gac      152
Tyr Leu Ala Asp Lys Ser Phe Trp Ala Glu Glu Leu Gln Asn Lys Asp
          20          25          30
acg gat ttt ggc tat tat caa aac aag cag ttt tta ttt gtg gct aat      200
Thr Asp Phe Gly Tyr Tyr Gln Asn Lys Gln Phe Leu Phe Val Ala Asn
          35          40          45          50
aaa tcc aag ccc agt ttg gag ttt tat gag ata gaa aat aac atg ctt      248
Lys Ser Lys Pro Ser Leu Glu Phe Tyr Glu Ile Glu Asn Asn Met Leu
          55          60          65
aaa aaa atc aac agc tct aaa gct ctt gta ggc tct aaa aag ggc gat      296
Lys Lys Ile Asn Ser Ser Lys Ala Leu Val Gly Ser Lys Lys Gly Asp
          70          75          80

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aag	act	tta	gag	ggc	gat	ttg	gcc	acg	cct	att	gga	gtg	tat	cgt	atc	344
Lys	Thr	Leu	Glu	Gly	Asp	Leu	Ala	Thr	Pro	Ile	Gly	Val	Tyr	Arg	Ile	
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acg	cag	aaa	tta	gag	cgc	ttg	gat	caa	tat	tat	ggc	gtt	ttg	gct	ttt	392
Thr	Gln	Lys	Leu	Glu	Arg	Leu	Asp	Gln	Tyr	Tyr	Gly	Val	Leu	Ala	Phe	
100105110																
gta	acg	aat	tac	cct	aat	ttg	tat	gat	acc	ttg	aaa	aaa	cgc	acc	ggg	440
Val	Thr	Asn	Tyr	Pro	Asn	Leu	Tyr	Asp	Thr	Leu	Lys	Lys	Arg	Thr	Gly	
115120125																
cat	ggc	att	tgg	gtg	cat	gga	atg	cct	tta	aat	ggc	gat	cgg	aat	gaa	488
His	Gly	Ile	Trp	Val	His	Gly	Met	Pro	Leu	Asn	Gly	Asp	Arg	Asn	Glu	
135140145																
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Leu	Asn	Thr	Lys	Gly	Cys	Ile	Ala	Ile	Glu	Asn	Pro	Leu	Leu	Ser	Ser	
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tat	gac	aaa	gtg	tta	aaa	ggc	gaa	aaa	gcg	ttc	ctc	atc	acc	tat	gaa	584
Tyr	Asp	Lys	Val	Leu	Lys	Gly	Glu	Lys	Ala	Phe	Leu	Ile	Thr	Tyr	Glu	
165170175																
gac	aag	ttt	ttc	cca	agc	acc	aaa	gaa	gaa	ttg	agc	atg	att	tta	agc	632
Asp	Lys	Phe	Phe	Pro	Ser	Thr	Lys	Glu	Glu	Leu	Ser	Met	Ile	Leu	Ser	
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Ser	Leu	Phe	Gln	Trp	Lys	Glu	Ala	Trp	Ala	Arg	Gly	Asp	Phe	Glu	Arg	
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Tyr	Met	Arg	Phe	Tyr	Asn	Pro	Asn	Phe	Thr	Arg	Tyr	Asp	Gly	Met	Lys	
215220225																
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Phe	Asn	Ala	Phe	Lys	Glu	Tyr	Lys	Lys	Arg	Val	Phe	Ala	Lys	Asn	Glu	
230235240																
aaa	aag	aat	atc	gct	ttt	tcc	tct	atc	aat	gtg	atc	cct	tac	ccc	aac	824
Lys	Lys	Asn	Ile	Ala	Phe	Ser	Ser	Ile	Asn	Val	Ile	Pro	Tyr	Pro	Asn	
245250255																
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Ser	Gln	Asn	Lys	Arg	Leu	Phe	Tyr	Val	Val	Phe	Asp	Gln	Asp	Tyr	Lys	
260265270																
gcc	tac	cag	cat	aac	aag	ctc	tct	tat	agc	tcc	aat	tct	caa	aaa	gaa	920
Ala	Tyr	Gln	His	Asn	Lys	Leu	Ser	Tyr	Ser	Ser	Asn	Ser	Gln	Lys	Glu	
275280285290																
ctc	tat	ata	gag	att	gaa	aac	aat	caa	gtg	tct	att	ata	atg	gaa	aaa	968
Leu	Tyr	Ile	Glu	Ile	Glu	Asn	Asn	Gln	Val	Ser	Ile	Ile	Met	Glu	Lys	
295300305																
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<210> 354
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 <212> PRT
 <213> Helicobacter pylori

<400> 354

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Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu Lys Thr Tyr Arg	
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Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser Asn Ile Thr Leu	
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gcc Ala	ata Ile	gag Glu	caa Gln	tgt Cys	tta Leu	gag Glu	ggc Gly	ttg Leu	agc Ser	gat Asp	agt Ser	gaa Glu	agg Arg	gcg Ala	cta Leu	1344

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gat cta aga aac cgt aaa acc ttt gat aac atg gcg gct aaa ggt tat	Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr	465	470	475	1440				
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aac gcc act aat gtt gat gcg gac aaa ata gct agc gat aat cct att	Asn Ala Thr Asn Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile	500	505	510	1536				
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acc att aag gat aag aat tta gaa gct aaa tta gct aag gct tta ggt	Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly	530	535	540	1632				
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gcc aag aat atc agt gaa atc gct ctt aag aac aaa aaa gaa aag agt	Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser	580	585	590	1776				
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act ctg act tct aaa gta gat gcc act ctc aca ggt ata gtg agt ggg	Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly	645	650	655	1968				
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Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe Leu Gln	
740 745 750	
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Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly Lys Gly	
755 760 765	
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Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly Asp Ser	
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Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys Gln Ser	
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acc aaa act ttg tct aga gaa cat gaa gaa atc acc aca agc ccc aaa	2592
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Asn Glu Ile Glu Leu Ala Leu Ile Arg Gly Asp Glu Asp Ala Lys Glu	
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Ile Leu Glu Lys Arg Leu Asp Lys Glu Val Lys Ser Ile Tyr Ser Asn	
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		35					40					45			
Thr	Asp	Phe	Gln	Lys	Leu	Gln	Leu	Ala	Arg	His	Pro	Asp	Arg	Pro	Tyr
	50					55					60				
Ala	Met	Asp	Tyr	Ile	Asp	Leu	Ile	Leu	Lys	Asp	Lys	Tyr	Glu	Val	Phe
65					70					75					80
Gly	Asp	Arg	His	Tyr	Asn	Asp	Asp	Lys	Ala	Ile	Val	Cys	Phe	Val	Gly
			85					90						95	
Lys	Ile	Asp	Asn	Val	Pro	Val	Val	Val	Ile	Gly	Glu	Glu	Lys	Gly	Arg
			100					105					110		
Gly	Thr	Lys	Asn	Lys	Leu	Leu	Arg	Asn	Phe	Gly	Met	Pro	Asn	Pro	Cys
		115					120					125			
Gly	Tyr	Arg	Lys	Ala	Leu	Lys	Met	Ala	Lys	Phe	Ala	Glu	Lys	Phe	Asn
		130				135					140				
Leu	Pro	Ile	Leu	Met	Leu	Val	Asp	Thr	Ala	Gly	Ala	Tyr	Pro	Gly	Ile
145				150						155					160
Gly	Ala	Glu	Glu	Arg	Gly	Gln	Ser	Glu	Ala	Ile	Ala	Lys	Asn	Leu	Gln
			165						170					175	
Glu	Phe	Ala	Ser	Leu	Lys	Val	Pro	Thr	Ile	Ser	Val	Ile	Ile	Gly	Glu
		180						185					190		
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<221> CDS

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Met	Gln	Phe	Thr	Gly	Lys	Asn	Val	Leu	Ile	Thr	Gly	Ala	Ser			
1				5					10							
aaa	ggc	att	ggg	gct	gaa	atc	gcc	aaa	act	ctc	gct	tct	atg	ggg	ctg	156
Lys	Gly	Ile	Gly	Ala	Glu	Ile	Ala	Lys	Thr	Leu	Ala	Ser	Met	Gly	Leu	
15					20					25					30	
aaa	ggt	tgg	atc	aat	tac	cgc	agt	aat	gct	gaa	gtg	gct	gac	gct	tgg	204
Lys	Val	Trp	Ile	Asn	Tyr	Arg	Ser	Asn	Ala	Glu	Val	Ala	Asp	Ala	Leu	
				35					40					45		
aaa	aat	gag	ctt	gaa	gaa	aaa	ggc	tat	aag	gca	gct	gtc	att	aaa	ttt	252

Lys	Asn	Glu	Leu	Glu	Gly	Lys	Gly	Tyr	Lys	Ala	Ala	Val	Ile	Lys	Phe
<div style="text-align:center;">50 55 60</div>															
gat	gcg	gct	tct	gaa	agc	gat	ttt	att	gaa	gcg	ata	caa	acc	atc	gtc
Asp	Ala	Ala	Ser	Glu	Ser	Asp	Phe	Ile	Glu	Ala	Ile	Gln	Thr	Ile	Val
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caa	agc	gat	ggg	ggg	ttg	tct	tac	ttg	gtg	aat	aac	gcc	ggg	gtg	gtg
Gln	Ser	Asp	Gly	Gly	Leu	Ser	Tyr	Leu	Val	Asn	Asn	Ala	Gly	Val	Val
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cgc	gat	aaa	tta	gcg	atc	aaa	atg	aaa	aca	gaa	gac	ttt	cac	cat	gtc
Arg	Asp	Lys	Leu	Ala	Ile	Lys	Met	Lys	Thr	Glu	Asp	Phe	His	His	Val
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ata	gac	aat	aac	ctc	act	tca	gcc	ttt	ata	ggg	tgc	cga	gag	gct	tta
Ile	Asp	Asn	Asn	Leu	Thr	Ser	Ala	Phe	Ile	Gly	Cys	Arg	Glu	Ala	Leu
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aag	gtg	atg	agc	aag	agt	cgt	ttt	ggg	agc	gtg	gtc	aat	gtc	gct	tct
Lys	Val	Met	Ser	Lys	Ser	Arg	Phe	Gly	Ser	Val	Val	Asn	Val	Ala	Ser
<div style="text-align:center;">130 135 140</div>															
atc	att	ggg	gaa	aga	ggc	aat	atg	ggg	cag	aca	aac	tac	tca	gcg	agt
Ile	Ile	Gly	Glu	Arg	Gly	Asn	Met	Gly	Gln	Thr	Asn	Tyr	Ser	Ala	Ser
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Lys	Gly	Gly	Met	Ile	Ala	Met	Ser	Lys	Ser	Phe	Ala	Tyr	Glu	Gly	Ala
<div style="text-align:center;">160 165 170</div>															
tta	agg	aat	att	cgt	ttc	aac	tct	gta	acg	ccc	ggg	ttt	ata	gaa	acc
Leu	Arg	Asn	Ile	Arg	Phe	Asn	Ser	Val	Thr	Pro	Gly	Phe	Ile	Glu	Thr
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gac	atg	aac	gcc	aat	ttg	aaa	gac	gaa	ctc	aaa	gcg	gat	tat	ggt	aaa
Asp	Met	Asn	Ala	Asn	Leu	Lys	Asp	Glu	Leu	Lys	Ala	Asp	Tyr	Val	Lys
<div style="text-align:center;">195 200 205</div>															
aac	att	cct	tta	aac	agg	cta	ggg	tct	gct	aag	gaa	gtg	gca	gaa	gcg
Asn	Ile	Pro	Leu	Asn	Arg	Leu	Gly	Ser	Ala	Lys	Glu	Val	Ala	Glu	Ala
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gta	ggg	ttc	ttt	tgagt	gat	cat	ctctag	tttac	atcact	gggag	agact	tct	caa		
Val	Xaa	Phe	Phe												
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Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu Lys Asn
 35 40 45
 Glu Leu Glu Glu Lys Gly Tyr Lys Ala Ala Val Ile Lys Phe Asp Ala
 50 55 60
 Ala Ser Glu Ser Asp Phe Ile Glu Ala Ile Gln Thr Ile Val Gln Ser
 65 70 75 80
 Asp Gly Gly Leu Ser Tyr Leu Val Asn Asn Ala Gly Val Val Arg Asp
 85 90 95
 Lys Leu Ala Ile Lys Met Lys Thr Glu Asp Phe His His Val Ile Asp
 100 105 110
 Asn Asn Leu Thr Ser Ala Phe Ile Gly Cys Arg Glu Ala Leu Lys Val
 115 120 125
 Met Ser Lys Ser Arg Phe Gly Ser Val Val Asn Val Ala Ser Ile Ile
 130 135 140
 Gly Glu Arg Gly Asn Met Gly Gln Thr Asn Tyr Ser Ala Ser Lys Gly
 145 150 155 160
 Gly Met Ile Ala Met Ser Lys Ser Phe Ala Tyr Glu Gly Ala Leu Arg
 165 170 175
 Asn Ile Arg Phe Asn Ser Val Thr Pro Gly Phe Ile Glu Thr Asp Met
 180 185 190
 Asn Ala Asn Leu Lys Asp Glu Leu Lys Ala Asp Tyr Val Lys Asn Ile
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 Pro Leu Asn Arg Leu Gly Ser Ala Lys Glu Val Ala Glu Ala Val Xaa
 210 215 220
 Phe Phe
 225

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 Met Pro Gly Ile
 1
 aag gtt aga gaa ggc gat gcg ttt gat gaa gct tat agg aga ttc aaa 162
 Lys Val Arg Glu Gly Asp Ala Phe Asp Glu Ala Tyr Arg Arg Phe Lys
 5 10 15 20
 aag caa acc gat cgc aat tta gtg gta aca gaa tgc cgt gct aga agg 210
 Lys Gln Thr Asp Arg Asn Leu Val Val Thr Glu Cys Arg Ala Arg Arg
 25 30 35
 ttc ttt gag tct aag act gaa aaa cgc aaa aaa caa aaa atc agc gct 258
 Phe Phe Glu Ser Lys Thr Glu Lys Arg Lys Lys Gln Lys Ile Ser Ala
 40 45 50
 aaa aag aag gtt ttg aag cgt ctt tat atg tta agg cgt tat gag tca 306
 Lys Lys Lys Val Leu Lys Arg Leu Tyr Met Leu Arg Arg Tyr Glu Ser
 55 60 65
 aga cta taatagactt taagaaaaat ttaaaaatta aggattattg aataatgcaa 362

Arg Leu
70

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373

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20 25 30
Arg Ala Arg Arg Phe Phe Glu Ser Lys Thr Glu Lys Arg Lys Lys Gln
35 40 45
Lys Ile Ser Ala Lys Lys Lys Val Leu Lys Arg Leu Tyr Met Leu Arg
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Arg Tyr Glu Ser Arg Leu
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23

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24

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<400> 367
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32

<210> 368
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<400> 368
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33